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Maximum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA:  
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2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq.\*  
3: /cgn2\_6/ptodata/2/ina/6\_COMB.seq.\*  
4: /cgn2\_6/ptodata/2/ina/PTUS\_COMB.seq.\*  
5: /cgn2\_6/ptodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No. Score Query Match Length DB ID Description

1 618 100.0 618 2 US-08-684-024-3 Sequence 3, Appli

2 618 100.0 618 3 US-09-145-868-3 Sequence 3, Appli

3 618 100.0 1484 2 US-08-684-024-5 Sequence 5, Appli

4 618 100.0 1484 3 US-09-145-868-5 Sequence 5, Appli

5 82.2 13.3 591 2 US-08-684-024-4 Sequence 4, Appli

6 82.2 13.3 591 3 US-09-145-868-4 Sequence 4, Appli

7 35.8 5.8 7218 1 US-08-232-463-14 Sequence 14, Appli

8 32.2 5.2 2694 1 US-08-465-995A-3 Sequence 3, Appli

9 32.2 5.2 2694 2 US-08-465-994C-3 Sequence 3, Appli

10 32.2 5.2 2694 2 US-08-966-145-3 Sequence 3, Appli

11 32.2 5.2 2760 1 US-08-101-593-3 Sequence 3, Appli

12 30.8 5.0 615 3 US-08-842-807A-22 Sequence 22, Appli

13 30.6 5.0 4500 2 US-08-743-637B-35 Sequence 35, Appli

14 30.6 5.0 4500 3 US-08-526-840B-35 Sequence 35, Appli

15 30.2 4.9 1659 3 US-09-083-351-3 Sequence 3, Appli

16 30.2 4.9 1959 3 US-09-166-460-1 Sequence 1, Appli

17 30.2 4.9 3946 3 US-09-083-351-1 Sequence 1, Appli

18 30 4.9 43676 3 US-09-356-952-12 Sequence 12, Appli

19 29.8 4.8 1060 1 US-08-850-118-1 Sequence 1, Appli

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21 29.8 4.8 1060 3 US-09-093-335-1 Sequence 1, Appli

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23 29.4 4.8 1194 3 US-08-929-329-3 Sequence 3, Appli

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28 29.2 4.7 1130 2 US-08-670-707A-3 Sequence 3, Appli

29 29.2 4.7 1130 4 PCT-US93-03275-1 Sequence 1, Appli  
30 29.2 4.7 1130 4 PCT-US94-13200-3 Sequence 3, Appli  
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33 29.2 4.7 1425 1 US-07-876-280-27 Sequence 27, Appli  
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36 29.2 4.7 1425 1 US-08-049-783-3 Sequence 3, Appli  
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41 29.2 4.7 1425 4 PCT-US92-03624-7 Sequence 7, Appli  
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43 29.2 4.7 1425 4 PCT-US93-07409-1 Sequence 1, Appli  
44 29.2 4.7 1623 1 US-08-121-202-3 Sequence 3, Appli  
45 29.2 4.7 2599 5 5266464-1 Patent No. 5266464

ALIGNMENTS

RESULT 1  
US-08-684-024-3  
Sequence 3, Application US/08684024  
Patent No. 5834298  
GENERAL INFORMATION:  
APPLICANT: Beneza, Robert  
TITLE OF INVENTION: GENE ENCODING THE HUMAN HOMOLOG OF MAD2  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham LLP  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/684,024  
FILING DATE: 19-JUL-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 1747/46621-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 278-0400  
TELEFAX: (212) 391-0526  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 618 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-684-024-3

Query Match 100.0%; Score 618; DB 2; Length 618;  
Best Local Similarity 100.0%; Pred. No. 1.7e-192;  
Matches 618; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 1 ATGGCGCTGCAGCTCTCCCGGAGGAGGAATCACCCCTGCGGGAGCGCCGAATCGTG 60  
QY 61 gccgagttcttcattcggcatcaacacatttatcagctggcgatatccatct 120

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## RESULT 2

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Sequence 3, Application US/09145868
Patent No. 6096522
GENERAL INFORMATION:
APPLICANT: Benezra, Robert
TITLE OF INVENTION: GENE ENCODING THE HUMAN HOMOLOG OF MAD2
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/145,868
FILING DATE: 02-SEP-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 1747/46621-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0526
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 618 base pairs
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-145-868-3
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Query Match 100.0%; Score 618; DB 3; Length 618;
Best Local Similarity 100.0%; Pred. No. 1.7e-192;
Matches 618; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 atggcgctgcagctctccgggagcagggaatcaccttgcgggagcgcgaaatcgtg 60
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Db 61 gccgagttcttcattcgggcatcaacagcattttatatcagcgtggtgcatatccatct 120
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Db 121 gaaacatttactcaggtgcagaaatcacgagctcaacttctgttgaactactgtattgag 180
Qy 181 ctcataaaatcctaaataatgtgtggaacacgaagattgtttacaaagtgttca 240
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Db 421 tttctgccactgtgtggaagtcttctgttcttctgttcttctgttcttctgttct 480
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Qy 541 gtgcgccttcgttcatttactactacacacaaagttaaatgacatgctggtccacaaa 600
Db 541 gtgcgccttcgttcatttactactacacacaaagttaaatgacatgctggtccacaaa 600
Qy 601 attcctgtcaatgactga 618
Db 601 attcctgtcaatgactga 618
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## RESULT 3

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Sequence 5, Application US/08684024
Patent No. 5834298
GENERAL INFORMATION:
APPLICANT: Benezra, Robert
TITLE OF INVENTION: GENE ENCODING THE HUMAN HOMOLOG OF MAD2
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/684.024  
FILING DATE: 19-JUL-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 1747/46621-A  
TELEPHONE: (212) 278-0400  
TELEFAX: (212) 391-0526  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1484 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 34...648  
US-08-684-024-5

Query Match 100.0%; Score 618; DB 2; Length 1484;  
Best Local Similarity 100.0%; Pred. No. 2.8e-192;  
Matches 618; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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2y	61	gccgagttctctcattcgcatcaacagcattttatcatcagctggcatatccatct	120
2b	94	GCCGAGTTCTCTCATTCGGCATCACAGCATTTTATATCAGCTGGCATATCCATCT	153
2y	121	gaaaccttactcagtgacagaaatcaggaactcaacctgcttgtaactactgattgag	180
2b	154	GAACCTTTACTCGAGTGCAGAAATACGACTCACCTTGTGTAACCTACTGATCTTGA	213
2y	181	ctcataaatacctaaataatgtgtggaacaactggaagattgtttatacaagtttca	240
2b	214	CTCATAAATACTAAATAATGTGTGGAACAACCTGAAAGATTGTTATACAAGTTTCA	273
2y	241	gttcagaactcagtgatgagttctgttcatttgcctgctgatttatacagacaaagt	300
2b	274	GTTCAAGAACTGGTTGTAGTTATCTCAATATTGAAGTGGTGAGTCTCGAAAGATGG	333
2y	301	cagtttgattgagtgacagactgcaaaagatgacagtgcacccagagaaagtct	360
2b	334	CAGTTTGATTGAGTGTGACAAAGATGCAAAAGATGACAGTGCACCCAGAGAAAGTCT	393
2y	361	cagaagctatccagatgaatacctcagtgatcacagatcacagctacggtgaca	420
2b	394	CAGAAGCTATCCAGATGAATACTCCGTTCAGTGATCAGACAGATCACAGTACGGTGACA	453
2y	421	ttctgcacactgttggaagttctgttcatttgcctgctgatttatacagacaaagt	480
2b	454	TTCTGCCACATGTTGGAGTTCTTGTTCATTGTTGATCTGCTGATTATACACAAAAGAT	513
2y	481	ttggttgactgaaataatgggaagctgggaccacagtttattaccaattctgagaa	540
2b	514	TGAGTTGTACCTGAAAAATGGAAGAGTGGGACACACAGTTTATTACCAATTTCTGAGAA	573
2y	541	gtgccttcgttcttactactcaaatcccaagaataatagcatggtgcctacaaa	600
2b	574	GTCGCCCTTCGTTCAATTACTACTACTCAATCCACAAGTAATAGCATGTTGTCCTACAAA	633
2y	601	attcctgtcaatgactga	618

Db 634 ATTCTGTCAATGACTGA 651

RESULT 4  
US-09-145-868-5  
Sequence 5, Application US/09145868  
Patent No. 6096522  
GENERAL INFORMATION:  
APPLICANT: Benezia, Robert  
TITLE OF INVENTION: GENE ENCODING THE HUMAN HOMOLOG OF MAD2  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham LLP  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/145,868  
FILING DATE: 02-SEP-1998  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 1747/46621-B  
TELEPHONE: (212) 278-0400  
TELEFAX: (212) 391-0526  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1484 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 34...648  
US-09-145-868-5

Query Match 100.0%; Score 618; DB 3; Length 1484;  
Best Local Similarity 100.0%; Pred. No. 2.8e-192;  
Matches 618; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	atggcgctgcagctctccgggagcagggaatcaacctgcgcgggagcgcaaatcgtg	60
Db	34	ATGGCGCTGCAGCTCTCCGGAGCAGGGAATCACCCCTGCGGGAGCGCGAAATCGT	93
Qy	61	gccagttctctcattcgcatcaacagcattttatcatcagctggcatatccatct	120
Db	94	GCCGAGTTCTCTCATTCGGCATCAACAGCATTTTATATCAGCTGGCATATCCATCT	153
Qy	121	gaaaccttactcagtgacagaaatcaggaactcaacctgcttgtaactactgattgag	180
Db	154	GAACCTTTACTCGAGTGCAGAAATACGACTCACCTTGTGTAACCTACTGATCTTGA	213
Qy	181	ctcataaatacctaaataatgtgtggaacaactggaagattgtttatacaagtttca	240
Db	214	CTCATAAATACTAAATAATGTGTGGAACAACCTGAAAGATTGTTATACAAGTTTCA	273
Qy	241	gttcagaactcagtgattgtgttattctcaaatgtggaagctggtcctggaagatgg	300
Db	274	GTTCAAGAACTGGTTGTAGTTATCTCAATATTGAAGTGGTGAGTCTCGAAAGATGG	333
Qy	301	cagtttgattgagtgacagactgcaaaagatgacagtgcacccagagaaagtct	360

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361 cagaaagctatccaggatgaataccgttcagtgatcagacagatcagacagctacgggtgaca 420  
394 CAGAAAGCTATCCAGGATGAATCCGTTTCAGTGATCAGACAGATCAGAGCTACGGTGACA 453  
421 ttctcgcaactgttggaagttcttctgttcatttgatctgctgatttatcacagacaagat 480  
454 TTTCTGCCACTGTGGAAAGTTCTTGTTCATTTCATCTGCTGATTTATACAGACAAGAT 513  
481 ttggtgtacctgaaataagggaagtcggaagtcggaccacagtttatcccaattctgagaa 540  
514 TTGGTGTACTGAAATAATGGGAGAGCTCGGACACAGTTTATTACCAATTTCTGAGAA 573  
541 gtgcgcttcgttcattactactataatccacaaagtaaatgacgtggtggcctacaaa 600  
574 GTGGCCTTCGTTCAATTACTACTACAAATCCACAAAGTAATAAGCATGCTGGCTACAAA 633  
601 attcctgtcaatgactga 618  
634 ATTCCTGTCAATGACTGA 651

RESULT 5  
US-08-684-024-4  
Sequence 4, Application US/08684024  
Patent No. 5834298  
GENERAL INFORMATION:  
APPLICANT: Beneza, Robert  
TITLE OF INVENTION: GENE ENCODING THE HUMAN HOMOLOG OF MAD2  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham LLP  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/684,024  
FILING DATE: 19-JUL-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 1747/46621-A  
TELEPHONE: (212) 278-0400  
TELEFAX: (212) 391-0526  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 591 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-684-024-4

Query Match 13.3%; Score 82.2; DB 2; Length 591;  
Best Local Similarity 49.5%; Pred. No. 2.1e-17;  
Matches 272; Conservative 0; Mismatches 268; Indels 9; Gaps 2;  
58 gtgcccaggtctctcattccgacacagcatttatatcagcgtgacatatacca 117  
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118 tctgaaaccttactcagtgagcagaatacggactcaccttctgttaactactgattt 177

100 GCAGAAGATTTCTAACGGTGAAGAGTACGATCTTACCTTACTAAAGACACATGATGAT 159  
178 gagctcataaaaacacataaatggtgggaacaaactgaaagattggttatatacaagtg 237  
160 GAACTGAAGATTTACATTCGGAATAATCTCTACAAGTTTCACAGGTTGGCTTCTTGTGGA 219  
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220 AATGCAATCAATTAGTATTATGTTAGTATGATGAGCAAGGATGAGGAGAGGTGTTGGAAGA 279  
298 tggcagttgatattgagtgacacagactgcaaaagatgacagtgacccagagagaaag 357  
280 TGTGCTTT---CAATGTCAACACATTTCTGCAATAGCAACGGGAGGATGATGTTGTA 336  
358 tctcagaagactcaccaggtgaaatccgttcagtgatcagacagatcagacagctacgg 417  
337 GATTTAAATACACAAATCACAATCAGAGCTTTTAATCAGGCAATCACCCTCAAGGTT 396  
418 acattctctgc-----actgttggaagttcttcttcatttgcattgctgctgattataca 471  
397 ACCTTTCTCCCGAATAAAGAAAGGTTGGGTACACATTCACAGTACTTGCATATACA 456  
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457 GACGCGGATGCTAAAGTTCGGTAGAATGGCGGACTCCCAATAGTAAGAGATACCTGAT 516  
532 tctgaggaagtcgcttcattactactataatccacaaagtaaatgacgtggtg 591  
517 GTGGAAGTAGTTCAATTCAAAACATTTCTTACCAAGCATCAATAAGTTGGTGGCAGGTC 576  
592 gctacaaa 600  
577 AGCTATAAA 585  
RESULT 6  
US-09-145-868-4  
Sequence 4, Application US/09145868  
Patent No. 6096522  
GENERAL INFORMATION:  
APPLICANT: Beneza, Robert  
TITLE OF INVENTION: GENE ENCODING THE HUMAN HOMOLOG OF MAD2  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham LLP  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/145,868  
FILING DATE: 02-SEP-1998  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 1747/46621-B  
TELEPHONE: (212) 278-0400  
TELEFAX: (212) 391-0526  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 591 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)  
US-09-145-868-4

Query Match 13.3%; Score 82.2; DB 3; Length 591;  
Best Local Similarity 49.5%; Pred. No. 2.1e-17;  
Matches 272; Conservative 0; Mismatches 268; Indels 9; Gaps 2;

```
2Y 58 gtggcgcaggtttcttcattcgcgcacacacagcattttatatacagcgtggcatatatacca 117
Db 40 GTTACAGAAATTTTCGATACAGCAATTAATTCATTTTGTACCAAGAGCGGTATACCCA 99
QY 118 tctgaacaccttactcagtcagagaatacgcactcacccttcttgtaactactatctt 177
Db 100 GCAGAAGATTTCGTACGGTGAAGAGTAGATCTTACGTTACTTAAGACACATGATGAT 159
QY 178 gagctcataaatacctataataatgtggtgggaacactgaaagattggtttatatacagtg 237
Db 160 GAACTGAAAGATTACATTCGGAAATTTCTTACAAAGTTCACAGGTGGCTTCTTGGTGGA 219
QY 238 tcagttcagaactcaggtgttagttatctcaaatattgaagtgtgagtccttggaaga 297
Db 220 AATGCAATCAATTAGTATTATGTATGTATGTAGACAAGGATCAGGAGAGGTGGTGAAGA 279
QY 298 tggcagtttgattgagtgtagaagactgcaaaagatgacagtcgacccagagaaaag 357
Db 280 TGTGCTT---CAATGTGCAACACATTTCTGCAATAGCAAGGGCAGGATGATGTGTA 336
QY 358 tctcagaagctatccaggtgaaatccgttcagtgatcagacagatcacagtcagtggt 417
Db 337 GATTTAATATACACACAAATCACAATCAGAGCTTTAATCAGGCAAAATCACCTCAACGGTT 396
QY 418 acatttctgcc-----actgttggaagttcttcttcttcttcttcttcttcttcttataca 471
Db 397 ACTTCTCTCCGCAACTACAAAGAGTGGGTACACATTCACAGTACTTGCATATACA 456
QY 472 gacaaagatttggttactgaaataatgggaagtcgggacacagctttattaccaat 531
Db 457 GACGGGATGCTAAGTTCGGTAGAATGGCGGACATCCAAATAGTAAAGAGATACCTGAT 516
QY 532 tctggaagtcgcttcgttcattactactatacacaatacacaataatagcatgtg 591
Db 517 GGTGAAGTAGTCAATTAACAAATCTCTTACCAAGCATATAAAGTTGGTGGCAGGTC 576
QY 592 gactacaaa 600
Db 577 AGCTATAAA 585
```

RESULT 7  
US-08-232-463-14/c  
Sequence 14, Application US/08232463  
Patent No. 5670367  
GENERAL INFORMATION:  
APPLICANT: DORNER, F.  
APPLICANT: SCHEIFLINGER, F.  
APPLICANT: FALKNER, F. G.  
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS  
NUMBER OF SEQUENCES: 52  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 1800 Diagonal Road, Suite 500  
CITY: Alexandria  
STATE: VA  
COUNTRY: USA  
ZIP: 22313-0299  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/232,463

```

;
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZgpt-Fls
; US-08-232-463-14

Query Match 5.8%; Score 35.8; DB 1; Length 7218;
Best Local Similarity 7.5%; Pred. No. 0.12;
Matches 19; Conservative 132; Mismatches 104; Indels 0; Gaps 0;

QY 186 aaatacctcaataatggttggaacactgaaagattggtttatatacagtcagttcagttca 245
Db 1283 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1224
QY 246 gaaactggttgtagttatctcaaatattgaaagtgtgagtcctctggaaagatggcagtt 305
Db 1223 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1164
QY 306 tgatattgagttgcaagactgcaaaagatgacagtcacccagagaaaagatctcagaa 365
Db 1163 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1104
QY 366 agctatcagatgaaatccgttcagtcagatcagacagatcagctagcgtgacatttct 425
Db 1103 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 404
QY 426 gccactgttggaagt 440
Db 1043 GCCAAGCTCGGAATT 1029
```

RESULT 8  
US-08-465-995A-3  
Sequence 3, Application US/08465995A  
Patent No. 5660980  
GENERAL INFORMATION:  
APPLICANT: Myron F. Goodman  
APPLICANT: Linda J. Renna-Krantz  
TITLE OF INVENTION: METHODS FOR IDENTIFYING AND ISOLATING  
TITLE OF INVENTION: VARIANT T4 POLYMERASES  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Robbins, Berliner & Carson, LLP  
STREET: 201 No. 5660980th Figueroa Street, Suite 500  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90012-2628  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: ASCII DOS/TEXT  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/465,995A  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Robert Berliner  
REGISTRATION NUMBER: 20,121  
REFERENCE/DOCKET NUMBER: 1920-305D2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 213/977-1001  
TELEFAX: 213/977-1003  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2694 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE: CDS  
LOCATION: 1..2694  
US-08-465-995A-3

Query Match 5.2%; Score 32.2; DB 1; Length 2694;  
Best Local Similarity 49.1%; Pred. No. 1.1;  
Matches 85; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

Y 174 tcttgagctcataaaatacctaaataatgtgtggaacaactgaaagattggtatacaa 233  
b 1291 TTTAAAGTTCATCCAAATTCATGAATATATCGCAGGAACAGCTCTAAACCGAGTGATGAA 1350  
Y 234 gtgttcagttcagaactgtgttagttatctcaaatattgaaagtgtgagtcctgga 293  
b 1351 TATTCTGTGTTCTCCGAATGGATGTATGATAAATCATCAAGAAGGTATCATTTCCAAAG 1410  
Y 294 aagatggcagttgtattgattgagtgacagactgcaaaagatgacagtgac 346  
b 1411 GAAATCGCTAAAGTATTTTCCACCGTAAGACCTGGAAAGAAAGAAATGTTCCG 1463

## RESULT 9

US-08-465-994C-3  
Sequence 3, Application US/08465994C  
Patent No. 5928919  
GENERAL INFORMATION:  
APPLICANT: MYRON F. GOODMAN  
APPLICANT: LINDA L. REHA-KRANTZ  
TITLE OF INVENTION: VARIANT DNA POLYMERASES  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Robbins, Berliner & Carson, LLP  
STREET: 201 No. 5928919th Figueroa Street, Suite 500  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90012-2628  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: ASCII DOS/TEXT  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/465,994C  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MARGARET A. CHURCHILL  
REGISTRATION NUMBER: 39,944  
REFERENCE/DOCKET NUMBER: 1920-305D1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 213/977-1001  
TELEFAX: 213/977-1003  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:

LENGTH: 2694 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE: CDS  
LOCATION: 1..2694  
US-08-465-994C-3

Query Match 5.2%; Score 32.2; DB 2; Length 2694;  
Best Local Similarity 49.1%; Pred. No. 1.1;  
Matches 85; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

QY 174 tcttgagctcataaaatacctaaataatgtgtggaacaactgaaagattggtatacaa 233  
Db 1291 TTTAAAGTTCATCCAAATTCATGAATATATCGCAGGAACAGCTCTAAACCGAGTGATGAA 1350  
QY 234 gtgttcagttcagaactgtgttagttatctcaaatattgaaagtgtgagtcctgga 293  
Db 1351 TATTCTGTGTTCTCCGAATGGATGTATGATAAATCATCAAGAAGGTATCATTTCCAAAG 1410  
QY 294 aagatggcagttgtattgattgagtgacagactgcaaaagatgacagtgac 346  
Db 1411 GAAATCGCTAAAGTATTTTCCACCGTAAGACCTGGAAAGAAAGAAATGTTCCG 1463

## RESULT 10

US-08-966-145-3  
Sequence 3, Application US/08966145A  
Patent No. 5945312  
GENERAL INFORMATION:  
APPLICANT: Goodman, Myron F.  
APPLICANT: Reha-Krantz, Linda J.  
TITLE OF INVENTION: Synthesis of Fluorophore-Labeled DNA  
FILE REFERENCE: 1920-353D1  
CURRENT APPLICATION NUMBER: US/08/966,145A  
EARLIER FILING DATE: 1997-11-07  
EARLIER APPLICATION NUMBER: US 08/632,742  
EARLIER FILING DATE: 1996-04-15  
NUMBER OF SEQ ID NOS: 4  
SEQ ID NO 3  
LENGTH: 2694 base pairs  
TYPE: DNA  
ORGANISM: T4 bacteriophage  
PUBLICATION INFORMATION:  
AUTHORS: Goodman, Myron F.  
AUTHORS: Reha-Krantz, Linda J.  
PATENT DOCUMENT NUMBER: US 5,660,980  
PATENT FILING DATE: 1995-06-06  
PUBLICATION DATE: 1997-08-26  
US-08-966-145-3

Query Match 5.2%; Score 32.2; DB 2; Length 2694;  
Best Local Similarity 49.1%; Pred. No. 1.1;  
Matches 85; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

QY 174 tcttgagctcataaaatacctaaataatgtgtggaacaactgaaagattggtatacaa 233  
Db 1291 TTTAAAGTTCATCCAAATTCATGAATATATCGCAGGAACAGCTCTAAACCGAGTGATGAA 1350  
QY 234 gtgttcagttcagaactgtgttagttatctcaaatattgaaagtgtgagtcctgga 293  
Db 1351 TATTCTGTGTTCTCCGAATGGATGTATGATAAATCATCAAGAAGGTATCATTTCCAAAG 1410  
QY 294 aagatggcagttgtattgattgagtgacagactgcaaaagatgacagtgac 346  
Db 1411 GAAATCGCTAAAGTATTTTCCACCGTAAGACCTGGAAAGAAAGAAATGTTCCG 1463

## RESULT 11

US-08-101-593-3

Sequence 3, Application US/08101593  
Patent No. 5547859

## GENERAL INFORMATION:

APPLICANT: Goodman, Myron F.  
APPLICANT: Reha-Krantz, Linda J.  
TITLE OF INVENTION: NEW DNA SEQUENCING ENZYMES  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:ADDRESSEE: Robbins, Berliner & Carspm  
STREET: 201 No. 5547859th Figueroa Street, Fifth Floor

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90012-2628

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/101,593

FILING DATE: 19930802

CLASSIFICATION: 436

## ATTORNEY/AGENT INFORMATION:

NAME: Spitals, John P.

REGISTRATION NUMBER: 29,215

REFERENCE/DOCKET NUMBER: 1920-305

TELEPHONE: (213) 977-1001

TELEFAX: (213) 977-1003

## INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 2760 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

FEATURE:

NAME/KEY: CDS

LOCATION: 1..2760

US-08-101-593-3

Query Match 5.2%; Score 32.2; DB 1; Length 2760;

Best Local Similarity 49.1%; Pred. NO. 1.1;

Matches 85; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

QY 174 tcttgagctcaataaataatgtgtgggaactgaagattggtataca 233

DB 1357 TTTAAAGTTCATCCATTATGATATATCGAGGACAGCTCTTAACCGAGTGATGAA 1416

QY 234 gtgttcagtcgaactggttagttatctcaaatattgaagtgtgagtcctgga 293

DB 1417 TATTCCTGTTCTCCGAATGATGATGATATAACATCAACAAGGTATCATTCCAAAG 1476

QY 294 aegatgagcttgatattgattgagtgacagactgcaaaagatgacagtgac 346

DB 1477 GAAATCGCTAAAGTATTTTCCAGCGTAAGACTGGAAAAAATAATGTTCCG 1529

## RESULT 12

US-08-642-807A-22

Sequence 22, Application US/08642807A

Patent No. 6087097

## GENERAL INFORMATION:

APPLICANT: Persing, D. H.

TITLE OF INVENTION: PCR DETECTION OF BORRELIA

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:

ADDRESSEE: Schwegman, Lundberg, Woessner &amp; Kluth, P.A.

STREET: P.O. Box 2938

CITY: Minneapolis

STATE: MN

COUNTRY: USA

ZIP: 55402

## COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 2.0

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/642,807A

FILING DATE: 03-MAY-1996

CLASSIFICATION: 435

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/241,496

FILING DATE: 12-MAY-1994

## ATTORNEY/AGENT INFORMATION:

NAME: Woessner, Warren D

REGISTRATION NUMBER: 30,440

REFERENCE/DOCKET NUMBER: 150.127051

## TELECOMMUNICATION INFORMATION:

TELEPHONE: 612-373-6900

TELEFAX: 612-339-3061

TELEX:

## INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:

LENGTH: 615 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: Genomic DNA

US-08-642-807A-22

Query Match 5.0%; Score 30.8; DB 3; Length 615;

Best Local Similarity 54.4%; Pred. NO. 1.3;

Matches 62; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 138 gcagaaatcaggactcaccttctgttaactactgattgagtcataaaataacataaa 197

DB 378 GGAGAAAGTAACAGCTAGCTTAATGACACTGACTGTGCTCAAGTACTAAAAAACTGGA 437

QY 198 taatgtgttggaacactgaagattggtatacaagtgttcagttcagaaact 251

DB 438 AATGGGATGCGGGACITCAACTTTAACAATTACGGTAACAGCAAAAAAACT 491

## RESULT 13

US-08-743-637B-35/c

Sequence 35, Application US/08743637B

Patent No. 5994066

## GENERAL INFORMATION:

APPLICANT: BERGERON, Michel G.

APPLICANT: PICARD, Francois J.

APPLICANT: OUELLETTE, Marc

APPLICANT: ROY, Paul H.

TITLE OF INVENTION: SPECIES-SPECIFIC AND UNIVERSAL DNA

TITLE OF INVENTION: PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND

TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED

TITLE OF INVENTION: ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...

NUMBER OF SEQUENCES: 273

## CORRESPONDENCE ADDRESS:

ADDRESSEE: QUARLES &amp; BRADY

STREET: 411 EAST WISCONSIN AVENUE

CITY: MILWAUKEE

STATE: WISCONSIN

COUNTRY: USA

ZIP: 53202-4497

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/743.637B
FILING DATE: 04-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/526.840
FILING DATE: 11-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: BAKER, Jean C.
REGISTRATION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 850586.90012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5000
TELEFAX: (414) 277-5591
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 4500 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Streptococcus pneumoniae
US-08-743-637B-35

Query Match          5.0%; Score 30.6; DB 2; Length 4500;
Best Local Similarity 50.3%; Pred. No. 4.6;
Matches 75; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

2y 161 ttgtaactactgattgagctcataaaatacctaaataatgtgtggaacaactgaaag 220
Db 1688 TTCAGTTCTTTAGTTATCTAGTTCACCTTGATATAATCAACTCTCTGACCATTGGAAGC 1629

2y 221 attggttatacaagtttcagttcagaaactggttagttatctcaaatattgaaagt 280
Db 1628 ATTGGTTTCAACATCTCTTTTCTATCACTGTTTCGACATTTTCCAAATCTCGTGCATA 1569

2y 281 gtgaggtctctggaagatggcagtttgat 309
Db 1568 GTAATCTCTTGGAAATTTTCTTCTTCTGCT 1540

RESULT 14
US-08-526-840B-35/c
Sequence 35, Application US/08526840B
Patent No. 6001564
GENERAL INFORMATION:
APPLICANT: BERGERON, Michel G.
APPLICANT: OUELLETTE, Marc
APPLICANT: ROY, Paul H.
TITLE OF INVENTION: SPECIFIC AND UNIVERSAL PROBES AND
TITLE OF INVENTION: AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY
TITLE OF INVENTION: COMMON BACTERIAL PATHOGENS AND ANTIBIOTIC RESISTANCE GENES
TITLE OF INVENTION: FROM CLINICAL SPECIMENS FOR ROUTINE DIAGNOSIS IN ...
NUMBER OF SEQUENCES: 177
CORRESPONDENCE ADDRESS:
ADDRESSEE: QUARLES & BRADY
STREET: 411 East Wisconsin Avenue
CITY: Milwaukee
STATE: Wisconsin
COUNTRY: USA
ZIP: 53202-4497
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/526.840B
FILING DATE: 11-SEP-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/304.732
FILING DATE: 12-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: BAKER, Jean C.
REGISTRATION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 850586.90012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5000
TELEFAX: (414) 277-5591
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 4500 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Streptococcus pneumoniae
US-08-526-840B-35

Query Match          5.0%; Score 30.6; DB 3; Length 4500;
Best Local Similarity 50.3%; Pred. No. 4.6;
Matches 75; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

Qy 161 ttgtaactactgattgagctcataaaatacctaaataatgtgtggaacaactgaaag 220
Db 1688 TTCAGTTCTTTAGTTATCTAGTTCACCTTGATATAATCAACTCTCTGACCATTGGAAGC 1629

Qy 221 attggttatacaagtttcagttcagaaactggttagttatctcaaatattgaaagt 280
Db 1628 ATTGGTTTCAACATCTCTTTTCTATCACTGTTTCGACATTTTCCAAATCTCGTGCATA 1569

Qy 281 gtgaggtctctggaagatggcagtttgat 309
Db 1568 GTAATCTCTTGGAAATTTTCTTCTTCTGCT 1540

RESULT 15
US-09-083-351-3
Sequence 3, Application US/09083351
Patent No. 6087107
GENERAL INFORMATION:
APPLICANT: Sheffield, Val C.
APPLICANT: Alward, Wallace L.M.
APPLICANT: Stone, Edwin M.
APPLICANT: Nishimura, Darryl
APPLICANT: Patil, Shiva
TITLE OF INVENTION: THERAPEUTICS AND DIAGNOSTICS FOR
TITLE OF INVENTION: CONGENITAL HEART DISEASE BASED ON A NOVEL HUMAN
TITLE OF INVENTION: TRANSCRIPTION FACTOR
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/083,351
FILING DATE: 22-MAY-1998
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: UIA-029.02
TELECOMMUNICATION INFORMATION:
```





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GenCore version 4.5  
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DM protein - protein search, using sw model

Run on: February 26, 2001, 15:00:31 ; Search time 11.92 seconds  
(without alignments)  
299,786 Million cell updates/sec

Title: US-09-352-570-2  
Perfect score: 1010  
Sequence: 1 REQGITLRGSAIEVAEFFSF.....FTTIHKVNSVAYKIPVND 199

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Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 174772

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/2/1aa/6\_COMB.pep:\*  
4: /cgn2\_6/ptodata/2/1aa/6\_COMB.pep:\*  
5: /cgn2\_6/ptodata/2/1aa/6\_COMB.pep:\*  
6: /cgn2\_6/ptodata/2/1aa/6\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1010	100.0	205	2	US-08-684-024-7
3	1010	100.0	205	3	US-09-145-868-1
4	1010	100.0	205	3	US-09-145-868-7
5	1003	99.3	205	2	US-08-684-024-6
6	1003	99.3	205	3	US-09-145-868-6
7	804.5	79.7	203	2	US-08-684-024-8
8	804.5	79.7	203	3	US-09-145-868-8
9	395.5	39.2	196	2	US-08-684-024-2
10	395.5	39.2	196	2	US-08-684-024-9
11	395.5	39.2	196	3	US-09-145-868-2
12	395.5	39.2	196	3	US-09-145-868-9
13	74	7.3	392	3	US-08-979-917A-2
14	72.5	7.2	418	1	US-08-261-206A-72
15	72.5	7.2	565	3	US-09-139-424-4
16	72	7.1	433	2	US-09-139-424-4
17	72	7.1	433	3	US-08-706-216-4
18	71	7.0	2233	2	US-08-569-853-1
19	71	7.0	2233	2	US-08-569-853-2
20	71	7.0	2233	3	US-08-987-439-1
21	70.5	7.0	182	3	US-08-691-563C-90
22	70.5	7.0	624	2	US-08-642-406A-22
23	70.5	7.0	773	3	US-08-434-000A-2
24	70	6.9	689	1	US-08-248-021A-2
25	69.5	6.9	1089	1	US-08-180-195-36
26	69.5	6.9	1089	1	US-08-477-329-36
27	69.5	6.9	1089	2	US-08-475-458-36
28	69.5	6.9	1089	3	US-08-980-400-36

29 68.5 6.8 215 2 US-08-935-396-10 Sequence 10, Appl  
30 68.5 6.8 378 2 US-08-986-217-6 Sequence 6, Appl  
31 68.5 6.8 380 2 US-09-028-587-4 Sequence 4, Appl  
32 68.5 6.8 380 2 US-09-227-420-4 Sequence 4, Appl  
33 68.5 6.8 539 3 US-08-941-445A-21 Sequence 13, Appl  
34 68.5 6.8 583 3 US-08-941-445A-13 Sequence 21, Appl  
35 68.5 6.8 593 2 US-08-987-466-1 Sequence 1, Appl  
36 68 6.7 431 2 US-08-928-613-2 Sequence 2, Appl  
37 68 6.7 431 3 US-09-193-524-2 Sequence 2, Appl  
38 68 6.7 432 1 US-07-698-926A-2 Sequence 2, Appl  
39 68 6.7 634 1 US-07-872-644-51 Sequence 51, Appl  
40 68 6.7 634 1 US-08-297-494-51 Sequence 51, Appl  
41 68 6.7 634 1 US-08-297-510-51 Sequence 51, Appl  
42 68 6.7 634 1 US-08-479-532-51 Sequence 51, Appl  
43 68 6.7 634 1 US-08-455-526-51 Sequence 51, Appl  
44 68 6.7 634 1 US-08-455-525-51 Sequence 51, Appl  
45 68 6.7 634 3 US-09-139-491-51 Sequence 51, Appl

ALIGNMENTS

RESULT 1  
US-08-684-024-1  
; Sequence 1, Application US/08684024  
; Patent No. 5834298  
; GENERAL INFORMATION:  
; APPLICANT: Benesira, Robert  
; TITLE OF INVENTION: GENE ENCODING THE HUMAN HOMOLOG OF MAD2  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper & Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/684,024  
; FILING DATE: 19-JUL-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 1747/46621-A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 278-0400  
; TELEFAX: (212) 391-0526  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 205 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-684-024-1

Query Match 100.0%; Score 1010; DB 2; Length 205;  
Best Local Similarity 100.0%; Pred. No. 2.6e-107;  
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 REQGITLRGSAIEVAEFFSFSGINSILYQGIYPSFTFRVQKYGLTLLVTTDLEIKYLN 60  
DB 7 REQGITLRGSAIEVAEFFSFSGINSILYQGIYPSFTFRVQKYGLTLLVTTDLEIKYLN 66  
QY 61 NVVEOLKDWLYKCSYQKLVVWISNIESGVLERWOFDECDKTAKDSDAPREKSOKAIOD 120

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b 67 NVVEQLKDWLYKCSVQKLVVVISNIESGEVLERWQFDIECDKTAKDSDAPREKSQKAIQD 126
y 121 EIRSVIRQITATVTFPLPVEVSCSFDLLIYTDKDLVPEKWEESGPGQFITNSEEVRLRSF 180
* b 127 EIRSVIRQITATVTFPLPVEVSCSFDLLIYTDKDLVPEKWEESGPGQFITNSEEVRLRSF 186
y 181 TTTTHKVNMSVAYKIPVND 199
b 187 TTTTHKVNMSVAYKIPVND 205

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```

RESULT 2
US-08-684-024-7
; Sequence 7, Application US/08684024
; Patent No. 5834298
; GENERAL INFORMATION:
; APPLICANT: Benzra, Robert
; TITLE OF INVENTION: GENE ENCODING THE HUMAN HOMOLOG OF MAD2
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/684,024
; FILING DATE: 19-JUL-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 1747/46621-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0526
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 205 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; S-08-684-024-7

```

```

Query Match 100.0%; Score 1010; DB 2; Length 205;
Best Local Similarity 100.0%; Pred. No. 2.6e-107;
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
y 1 REQGITLRGSAEIVAEFFSGINSILYQGIYPSSETFTRVQKYGILTLVTTDLELIYLN 60
b 7 REQGITLRGSAEIVAEFFSGINSILYQGIYPSSETFTRVQKYGILTLVTTDLELIYLN 66
y 61 NVVEQLKDWLYKCSVQKLVVVISNIESGEVLERWQFDIECDKTAKDSDAPREKSQKAIQD 120
b 67 NVVEQLKDWLYKCSVQKLVVVISNIESGEVLERWQFDIECDKTAKDSDAPREKSQKAIQD 126
y 121 EIRSVIRQITATVTFPLPVEVSCSFDLLIYTDKDLVPEKWEESGPGQFITNSEEVRLRSF 180
b 127 EIRSVIRQITATVTFPLPVEVSCSFDLLIYTDKDLVPEKWEESGPGQFITNSEEVRLRSF 186
y 181 TTTTHKVNMSVAYKIPVND 199
b 187 TTTTHKVNMSVAYKIPVND 205

```

```

RESULT 4
US-09-145-868-7
; Sequence 7, Application US/09145868
; Patent No. 6096522
; GENERAL INFORMATION:
; APPLICANT: Benzra, Robert
; TITLE OF INVENTION: GENE ENCODING THE HUMAN HOMOLOG OF MAD2
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas

```

```

Query Match 100.0%; Score 1010; DB 2; Length 205;
Best Local Similarity 100.0%; Pred. No. 2.6e-107;
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
y 1 REQGITLRGSAEIVAEFFSGINSILYQGIYPSSETFTRVQKYGILTLVTTDLELIYLN 60
b 7 REQGITLRGSAEIVAEFFSGINSILYQGIYPSSETFTRVQKYGILTLVTTDLELIYLN 66
y 61 NVVEQLKDWLYKCSVQKLVVVISNIESGEVLERWQFDIECDKTAKDSDAPREKSQKAIQD 120
b 67 NVVEQLKDWLYKCSVQKLVVVISNIESGEVLERWQFDIECDKTAKDSDAPREKSQKAIQD 126
y 121 EIRSVIRQITATVTFPLPVEVSCSFDLLIYTDKDLVPEKWEESGPGQFITNSEEVRLRSF 180
b 127 EIRSVIRQITATVTFPLPVEVSCSFDLLIYTDKDLVPEKWEESGPGQFITNSEEVRLRSF 186
y 181 TTTTHKVNMSVAYKIPVND 199
b 187 TTTTHKVNMSVAYKIPVND 205

```

```

RESULT 3
US-09-145-868-1
; Sequence 1, Application US/09145868
; Patent No. 6096522
; GENERAL INFORMATION:
; APPLICANT: Benzra, Robert
; TITLE OF INVENTION: GENE ENCODING THE HUMAN HOMOLOG OF MAD2
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas

```

```

Query Match 100.0%; Score 1010; DB 3; Length 205;
Best Local Similarity 100.0%; Pred. No. 2.6e-107;
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
y 1 REQGITLRGSAEIVAEFFSGINSILYQGIYPSSETFTRVQKYGILTLVTTDLELIYLN 60
b 7 REQGITLRGSAEIVAEFFSGINSILYQGIYPSSETFTRVQKYGILTLVTTDLELIYLN 66
y 61 NVVEQLKDWLYKCSVQKLVVVISNIESGEVLERWQFDIECDKTAKDSDAPREKSQKAIQD 120
b 67 NVVEQLKDWLYKCSVQKLVVVISNIESGEVLERWQFDIECDKTAKDSDAPREKSQKAIQD 126
y 121 EIRSVIRQITATVTFPLPVEVSCSFDLLIYTDKDLVPEKWEESGPGQFITNSEEVRLRSF 180
b 127 EIRSVIRQITATVTFPLPVEVSCSFDLLIYTDKDLVPEKWEESGPGQFITNSEEVRLRSF 186
y 181 TTTTHKVNMSVAYKIPVND 199
b 187 TTTTHKVNMSVAYKIPVND 205

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CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/145,868  
FILING DATE: 02-SEP-1998  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 1747/46621-B  
TELEPHONE: (212) 278-0400  
TELEFAX: (212) 391-0526  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 205 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-145-868-7

Query Match 100.0%; Score 1010; DB 3; Length 205;  
Best-Local Similarity 100.0%; Pred. No. 2.6e-107; Indels 0; Gaps 0;  
Matches 199; Conservative 0; Mismatches 0;

QY 1 REQGITLRGSAEIVAEFFSGINSILYQRIYPSFTFTRVQYGLTLLVTTDLEIKYLN 60  
|||||  
DB 7 REQGITLRGSAEIVAEFFSGINSILYQRIYPSFTFTRVQYGLTLLVTTDLEIKYLN 66  
|||||

QY 61 NVVEQLKDWLYKCSVQKLVVVISNIESGEVLERWQFDIECDKTAKDSDAPREKSQKAIOD 120  
|||||  
DB 67 NVVEQLKDWLYKCSVQKLVVVISNIESGEVLERWQFDIECDKTAKDSDAPREKSQKAIOD 126  
|||||

QY 121 EIRSVIRQITATVTFPLLEVSCFDLLIYTDKLVVPEKWEESGPGQFTINSEEVRLRSF 180  
|||||  
DB 127 EIRSVIRQITATVTFPLLEVSCFDLLIYTDKLVVPEKWEESGPGQFTINSEEVRLRSF 186  
|||||

QY 181 TTTIHKVNSWYKIPVND 199  
|||||  
DB 187 TTTIHKVNSWYKIPVND 205  
|||||

RESULT 5  
US-08-684-024-6  
Sequence 6, Application US/08684024  
Patent No. 5834298  
GENERAL INFORMATION:  
APPLICANT: Benezra, Robert  
TITLE OF INVENTION: GENE ENCODING THE HUMAN HOMOLOG OF MAD2  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham LLP  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/684,024

FILING DATE: 19-JUL-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 1747/46621-A  
TELEPHONE: (212) 278-0400  
TELEFAX: (212) 391-0526  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 205 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-684-024-6

Query Match 99.3%; Score 1003; DB 2; Length 205;  
Best-Local Similarity 99.5%; Pred. No. 1.6e-106; Indels 0; Gaps 0;  
Matches 198; Conservative 0; Mismatches 1;

QY 1 REQGITLRGSAEIVAEFFSGINSILYQRIYPSFTFTRVQYGLTLLVTTDLEIKYLN 60  
|||||  
DB 7 REQGITLRGSAEIVAEFFSGINSILYQRIYPSFTFTRVQYGLTLLVTTDLEIKYLN 66  
|||||

QY 61 NVVEQLKDWLYKCSVQKLVVVISNIESGEVLERWQFDIECDKTAKDSDAPREKSQKAIOD 120  
|||||  
DB 67 NVVEQLKDWLYKCSVQKLVVVISNIESGEVLERWQFDIECDKTAKDSDAPREKSQKAIOD 126  
|||||

QY 121 EIRSVIRQITATVTFPLLEVSCFDLLIYTDKLVVPEKWEESGPGQFTINSEEVRLRSF 180  
|||||  
DB 127 EIRSVIRQITATVTFPLLEVSCFDLLIYTDKLVVPEKWEESGPGQFTINSEEVRLRSF 186  
|||||

QY 181 TTTIHKVNSWYKIPVND 199  
|||||  
DB 187 TTTIHKVNSWYKIPVND 205  
|||||

RESULT 6  
US-09-145-868-6  
Sequence 6, Application US/09145868  
Patent No. 6096522  
GENERAL INFORMATION:  
APPLICANT: Benezra, Robert  
TITLE OF INVENTION: GENE ENCODING THE HUMAN HOMOLOG OF MAD2  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham LLP  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/145,868  
FILING DATE: 02-SEP-1998  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 1747/46621-B  
TELEPHONE: (212) 278-0400  
TELEFAX: (212) 391-0526  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 205 amino acids

TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
S-09-145-868-6

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Query Match      99.3%; Score 1003; DB 3; Length 205;
Best Local Similarity 99.5%; Pred. No. 1.6e-106;
Matches 198; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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1 REGGITLRGSAEIVAEFFFGINSILYQRIQIYPSEFTFRVQRYGLTLVTTDLEIKLYN 60  
|||||  
|||||

7 REGGITLRGSAEIVAEFFFGINSILYQRIQIYPSEFTFRVQRYGLTLVTTDLEIKLYN 66  
|||||  
|||||

61 NVVEQLKDWLYKCSVKLVVVVISNIESGEVLERWOFIDECDTAKDDSAPREKSQAIOQ 120  
|||||  
|||||

67 NVVEQLKDWLYKCSVKLVVVVISNIESGEVLERWOFIDECDTAKDDSAPREKSQAIOQ 126  
|||||  
|||||

121 EIRSVIRQTATVTFLPPLLEVSCSPDLLITYTDKLWVPKEWESGPQFITNSEEVRLRSF 180  
|||||  
|||||

127 EIRSVIRQTATVTFLPPLLEVSCSPDLLITYTDKLWVPKEWESGPQFITNSEEVRLRSF 186  
|||||  
|||||

181 TTTTHKVNSVMAYKIPVD 199  
|||||  
|||||

187 TTTTHKVNSVMAYKIPVD 205  
|||||  
|||||

RESULT 7  
 S-08-684-024-8  
 Sequence 8, Application US/08684024  
 Patent No. 5834298  
 GENERAL INFORMATION:  
 APPLICANT: Benezra, Robert  
 TITLE OF INVENTION: GENE ENCODING THE HUMAN HOMOLOG OF MAD2  
 NUMBER OF SEQUENCES: 9  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Cooper & Dunham LLP  
 STREET: 1185 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: U.S.A.  
 ZIP: 10036  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/684,024  
 FILING DATE: 19-JUL-1996  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: White, John P.  
 REGISTRATION NUMBER: 28,678  
 REFERENCE/DOCKET NUMBER: 1747/46621-A  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 278-0400  
 TELEFAX: (212) 391-0526  
 INFORMATION FOR SEQ ID NO: 8:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 203 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 S-08-684-024-8

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Db      8  EGTLLKGSAEIVSEFFCGINSILYQGIYPSETFTIRQKYGLTLVLVSTDPAKLEYLNKV  67
QY      63  VEOLKDWLYKCSQKLVVVISNIESGEVLERWQFQIEDCKTAKDDSAAPREKSQKAIQDEI  122
Db      68  TDOLKDWLYKCSQKLVVVISNIDSNEILRWQFQIEDCKTVK-DGIVVREKSQKVIQEEI  126
QY      123  RSVIRQITATVTFPLPLEVSCSFDLLIYTDKDLVPEKWEESGPOFIINSEEVRLRSTTT  182
Db      127  RSVIRQITATVTFPLPLETACAFDILLIYTDKDLVPEKWEESGPOFVNSNEEVRLRSTTT  186
QY      183  TIHKVNSMVAYK 194
Db      187  TIHKVNSMVAYK 198

RESULT      8
US-09-145-868-8
; Sequence 8, Application US/09145868
; Patent No. 6096522
; GENERAL INFORMATION:
; APPLICANT: Benezira, Robert
; TITLE OF INVENTION: GENE ENCODING THE HUMAN HOMOLOG OF MAD2
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/145,868
; FILING DATE: 02-SEP-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 1747/46621-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0526
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 203 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SS-09-145-868-8

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2Y 183 TIKKNSMVAYK 194  
Db 187 TIKKNSMVAYK 198

RESULT 9

JS-08-684-024-2  
Sequence 2, Application US/08684024  
Patent No. 5834298

GENERAL INFORMATION:

APPLICANT: Beneza, Robert

TITLE OF INVENTION: GENE ENCODING THE HUMAN HOMOLOG OF MAD2

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: Cooper & Dunham LLP  
STREET: 1185 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/684,024

FILING DATE: 19-JUL-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: White, John P.

REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 1747/46621-A

TELEPHONE: (212) 278-0400

TELEFAX: (212) 391-0526

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 196 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

JS-08-684-024-2

Query Match 39.2%; Score 395.5; DB 2; Length 196;

Best Local Similarity 43.1%; Pred. No. 2.4e-37;

Matches 85; Conservative 37; Mismatches 66; Indels 9; Gaps 3;

2Y 3 QGITLRGSAEIVAEFFSGINSILYQRYGYPSETFTRVQKYGLTLVTTDLLEIKYLN 62  
Db 3 QSISLKGSTRTVTEFFEYSINSILYQRYGYPSETFTRVQKYGLTLVTTDLLEIKY 62

2Y 63 VEQLKDWLYKCSQKLVVVISNESGEVLERWQFDIE---CDKTKADDSAPREKSKQAIQ 119  
Db 63 LIQVHRWLGGKNCQLVLCIVDKDEGEVVERWFSNVQHISGNSGQDDVV---DLNTTQ 118

2Y 120 DEIRSVIROITATVTFPLPL--EVSCSFLLIYTDKLVVPEKWEESGPGQFITNSEVRL 177  
Db 119 SQIRALIROITSSVTFPELTKEGGYTFVLTADAKVPLEWADSNKSEIKPDGEVVQF 178

2Y 178 RSFTTTHKVNMSVAYK 194  
Db 179 KTFSTNDHKVGAQVSYK 195

RESULT 10  
JS-08-684-024-9  
Sequence 9, Application US/08684024  
Patent No. 5834298

GENERAL INFORMATION:

APPLICANT: Beneza, Robert

TITLE OF INVENTION: GENE ENCODING THE HUMAN HOMOLOG OF MAD2

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: Cooper & Dunham LLP  
STREET: 1185 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

TITLE OF INVENTION: GENE ENCODING THE HUMAN HOMOLOG OF MAD2

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: Cooper & Dunham LLP  
STREET: 1185 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/684,024

FILING DATE: 19-JUL-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: White, John P.

REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 1747/46621-A

TELEPHONE: (212) 278-0400

TELEFAX: (212) 391-0526

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 196 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-684-024-9

Query Match 39.2%; Score 395.5; DB 2; Length 196;

Best Local Similarity 43.1%; Pred. No. 2.4e-37;

Matches 85; Conservative 37; Mismatches 66; Indels 9; Gaps 3;

QY 3 QGITLRGSAEIVAEFFSGINSILYQRYGYPSETFTRVQKYGLTLVTTDLLEIKYLN 62  
Db 3 QSISLKGSTRTVTEFFEYSINSILYQRYGYPSETFTRVQKYGLTLVTTDLLEIKY 62

QY 63 VEQLKDWLYKCSQKLVVVISNESGEVLERWQFDIE---CDKTKADDSAPREKSKQAIQ 119  
Db 63 LIQVHRWLGGKNCQLVLCIVDKDEGEVVERWFSNVQHISGNSGQDDVV---DLNTTQ 118

QY 120 DEIRSVIROITATVTFPLPL--EVSCSFLLIYTDKLVVPEKWEESGPGQFITNSEVRL 177  
Db 119 SQIRALIROITSSVTFPELTKEGGYTFVLTADAKVPLEWADSNKSEIKPDGEVVQF 178

QY 178 RSFTTTHKVNMSVAYK 194  
Db 179 KTFSTNDHKVGAQVSYK 195

RESULT 11  
US-09-145-868-2  
Sequence 2, Application US/09145868  
Patent No. 6096522

GENERAL INFORMATION:

APPLICANT: Beneza, Robert

TITLE OF INVENTION: GENE ENCODING THE HUMAN HOMOLOG OF MAD2

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: Cooper & Dunham LLP  
STREET: 1185 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk





SEQUENCE CHARACTERISTICS:  
LENGTH: 392 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: No. 6118050e  
US-08-979-917A-2

Query Match 7.3%; Score 74; DB 3; Length 392;  
Best Local Similarity 19.8%; Pred. No. 2.8;  
Matches 48; Conservative 38; Mismatches 77; Indels 80; Gaps 12;  
QY 9 GSAEIVAEFF--SPGINSILYQRIYPS--ETFTRVQKYGTLTVDLLEIKLVNVE 64  
DB 27 GNAQAASFCYCNKMGFFLEAY-RGLETSREVSVHVKRGKIVFV-----LCSALNPWK 80  
2Y 65 QLKDWLYKCSVQKLVVVISNIESGEVLEWQFQIE-CDKTAQDSDAPREKSAIQ----- 119  
DB 81 EMGDHLVK-----GDGVKDIAFEVEDCDHIVQ---KARERCAKIVREPWF 122  
2Y 120 -----DEIRSVIRQIATVTFPLPLEV-----SCSFDDLII 150  
DB 123 EQDKFGKVKFAVLQYGDTHTLVEKINYTGRLPGFPEAPYKDTLLPKLPRCNLEIIDH 182  
QY 151 -----TKDKLVVPEKWESEGPQF-----ITNSEVRLRSEFTTHHKVNSWVAYKIP 196  
DB 183 IVGNQPDQMSQASEWYLNQLFHFWSDVDQVHTYISLSRIVVT-----NYESIKMP 238  
2Y 197 VND 199  
DB 239 INE 241

RESULT 14  
US-08-261-206A-72  
Sequence 72, Application US/08261206A  
Patent No. 5574007  
GENERAL INFORMATION:  
APPLICANT: Zushi, Mitichitaka  
APPLICANT: Gomi, Komakazu  
APPLICANT: Yamamoto, Shuji  
APPLICANT: Suzuki, Koji  
APPLICANT: Matsuda, Akio  
TITLE OF INVENTION: A Polypeptide Capable of Interacting  
TITLE OF INVENTION: with Thrombin  
NUMBER OF SEQUENCES: 80  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Birch, Stewart, Kolasch & Birch  
STREET: 301 N. Washington St.  
CITY: Falls Church  
STATE: Virginia  
COUNTRY: USA  
ZIP: 22046-0747  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/261,206A  
FILING DATE:  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/740,492  
FILING DATE: 03-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Svensson, Leonard R.  
REGISTRATION NUMBER: 30330  
REFERENCE/DOCKET NUMBER: 216-275P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-241-1300  
TELEFAX: 703-241-2848

TELEX: 248345  
INFORMATION FOR SEQ ID NO: 72:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 418 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-261-206A-72

Query Match 7.2%; Score 72.5; DB 1; Length 418;  
Best Local Similarity 32.1%; Pred. No. 4.5;  
Matches 27; Conservative 12; Mismatches 36; Indels 9; Gaps 3;  
QY 42 KYGLTLLVTTDLLEIKLVNVEQLDWLYKCSVQKLVVVISNIESGEV--LERWQFDIE 99  
DB 75 KYSLOPVVP---ELEKLLGKSVTFAPD---CVGAEEVGIVAKADGAVVLLLENLFHIE 127  
QY 100 CDKTAQDSDAPREKSKAKIODEIR 123  
DB 128 EGSAKDKGNKTKADKAKVDEFR 151

RESULT 15  
US-08-961-083-218  
Sequence 218, Application US/08961083  
Patent No. 6159469  
GENERAL INFORMATION:  
APPLICANT: Choi et. al.  
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines  
NUMBER OF SEQUENCES: 452  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: Maryland  
COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
COMPUTER: HP Vectra 486/33  
OPERATING SYSTEM: MSDOS version 6.2  
SOFTWARE: ASCII Text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/961,083  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Brookes, A. Anders  
REGISTRATION NUMBER: 36,373  
REFERENCE/DOCKET NUMBER: PB340P2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (301) 309-8504  
TELEFAX: (301) 309-8512  
INFORMATION FOR SEQ ID NO: 218:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 565 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-961-083-218  
Query Match 7.2%; Score 72.5; DB 3; Length 565;  
Best Local Similarity 19.9%; Pred. No. 7;  
Matches 34; Conservative 37; Mismatches 69; Indels 31; Gaps 8;  
QY 29 RGIYPSFTFRVQKYGTLVTTDLLEIKY---LNNVSEQLDWLYKCSVQKLVVVISN 84

2b 278 KGVYASEPVKQPEVNSEINKLKTALNVDKTELNNTIADAK-----TK 322  
2y 85 IESGEVLERWQFDIECDKTAKDDSAPEKSKQAIODEIRSVIRQITATVTFLLPLEVSCS 144  
3 323 VKEHYSDRSWQ-NLQTEVTKAEKVA---ANTDAKQSEVNEAVEKLTATIE--KLVELS-E 375  
y 145 FDLIYTDKDLVVPKWEESGPGQFITNSEEVRLRSFTTIIHK---VNSMV 191  
b 376 KPILTLTSTDKKILER-EAVAKYTLENQNKTKIKSITAEKKGEEVINIVV 425

Search completed: February 26, 2001, 15:03:32  
Job time: 181 sec



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419 CATTCTGCCACTGTGGAGTTTCTTGTTCATTTGATCTGCTGATTAT 468
151 ThrAspLysAspLeuValProGluLysTrpGluSerGlyProG1 167
469 ACAGACAAAGATTGTTGTTACCTGAAATAATGGAAGAGTCGGACCACA 518
167 nPheIleThrAsnSerGluGluValArgLeuArgSerPheThrThrI 184
519 GTTTATTACCAATTCAGGAAGTCGCTTCGTTTCATTTACTACTACAA 568
184 IeHisLysValAsnSerMetValAlaIleLysIleProValAsnAsp 199
569 TCCACAAAGTAATAGCATGGTGGCTACAAAATTCCTGTCATGAC 615
-seq_name: /cgn2_6/ptodata/2/pna/US6017_COMB.seq:US-60-172-360-24154
seq_documentation_block:
; Sequence 24154, Application US/60172360
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Lal, Preeti
; APPLICANT: Diep, Dinh
; TITLE OF INVENTION: Polynucleotide Sequence Polymorphisms Using
; FILE REFERENCE: GX-0007 P
; CURRENT APPLICATION NUMBER: US/60/172,360
; CURRENT FILING DATE: 1999-12-16
; NUMBER OF SEQ ID NOS: 29838
; SOFTWARE: PERL Program
; SEQ ID NO 24154
; LENGTH: 1505
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 199471.2
S-60-172-360-24154
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alignment_scores:
  Quality: 1010.00      Length: 199
  Ratio: 5.075          Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
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alignment_block:
US-09-352-570-2 x US-60-172-360-24154
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Align seg 1/1 to: US-60-172-360-24154 from: 1 to: 1505
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1 ArgGluGlnGlyIleThrLeuArgGlySerAlaGluIleValAlaGluPh 17
210 CGGGAGCAGGGAATCACCCTCGCGGGAGCGCCGAAATCGTGGCCGAGTT 259
17 ePheSerPheGlyIleAsnSerIleLeuTrpGlnArgGlyIleTrpPro 34
260 CTCTCATTCGSCATCAACAGCAATTTATATACAGCGTGCATATATCCAT 309
34 erGluThrPheThrArgValGlnLysTrpGlyLeuThrLeuValThr 50
310 CTGAACACCTTTACGAGTGCAGAAATACGGACTCACCTTGTGTAAC 359
51 ThrAspLeuGluLeuIleLysTrpLeuAsnValValGluGlnLeuLy 67
360 ACTGATCTGAGCTCATAAATACCTAATATGTTGGTGGAACTACTGA 409
67 sAspTrpLeuTrpLysCysSerValGlnLysLeuValValIleSera 84
410 AGATTGGTTATACAGTCTTCAGTTCAGAACTGGTTCTAGTATCTCAA 459
84 snIleGluSerGlyGluValLeuGluArgTrpGlnPheAspIleGluCys 100
460 ATATTGAAAGTGGTGGAGTCTCTGGAAGATGCGAGTTTCATATTGAGTGT 509
```

```
101 AspLysThrAlaLysAspSerAlaProArgGluLysSerGlnLysAl 117
510 GACAAGACTGCAAAAGATGACAGTGCACCCAGAGAAAGTCTCAGAAAGC 559
117 aiIeGlnAspGluIleArgSerValIleArgGlnIleThrAlaThrValT 134
560 TATCCAGGATGAATCCGTTTCAGTGCATGATCAGACATCACAGCTACGGTGA 609
134 hrPheLeuProLeuLeuGluValSerCysSerPheAspLeuLeuIleTrp 150
610 CATTCTGCCACTGTGGAGTTTCTTGTTCATTTGATCTGCTGATTAT 659
151 ThrAspLysAspLeuValProGluLysTrpGluSerGlyProG1 167
660 ACAGACAAAGATTGTTGTTACCTGAAATAATGGAAGAGTCGGACCACA 709
167 nPheIleThrAsnSerGluGluValArgLeuArgSerPheThrThrI 184
710 GTTTATTACCAATTCAGGAAGTCGCTTCGTTTCATTTACTACTACAA 759
184 IeHisLysValAsnSerMetValAlaIleLysIleProValAsnAsp 199
760 TCCACAAAGTAATAGCATGGTGGCTACAAAATTCCTGTCATGAC 806
seq_name: /cgn2_6/ptodata/2/pna/US6019_COMB.seq:US-60-195-106-210
seq_documentation_block:
; Sequence 210, Application US/60195106
; GENERAL INFORMATION:
; APPLICANT: Shiffman, Dov
; APPLICANT: Somogyi, Roland
; APPLICANT: Lawn, Richard M.
; APPLICANT: Sellhammer, Jeffrey J.
; APPLICANT: Porter, Gordon J.
; APPLICANT: Mikita, Thomas
; APPLICANT: Tai, Julie T.N.
; TITLE OF INVENTION: GENES EXPRESSED IN FOAM CELL DIFFERENTIATION
; FILE REFERENCE: PA-0025 P
; CURRENT APPLICATION NUMBER: US/60/195,106
; CURRENT FILING DATE: 2000-04-05
; NUMBER OF SEQ ID NOS: 276
; SOFTWARE: PERL Program
; SEQ ID NO 210
; LENGTH: 1505
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 199471.2
US-60-195-106-210
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alignment_scores:
  Quality: 1010.00      Length: 199
  Ratio: 5.075          Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
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alignment_block:
US-09-352-570-2 x US-60-195-106-210
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Align seg 1/1 to: US-60-195-106-210 from: 1 to: 1505
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1 ArgGluGlnGlyIleThrLeuArgGlySerAlaGluIleValAlaGluPh 17
210 CGGGAGCAGGGAATCACCCTCGCGGGAGCGCCGAAATCGTGGCCGAGTT 259
17 ePheSerPheGlyIleAsnSerIleLeuTrpGlnArgGlyIleTrpPro 34
260 CTCTCATTCGSCATCAACAGCAATTTATATACAGCGTGCATATATCCAT 309
34 erGluThrPheThrArgValGlnLysTrpGlyLeuThrLeuValThr 50
310 CTGAACACCTTTACTCGAGTGCAGAAATACGGACTCACCTTGTGTAAC 359
```

```

51 ThrAspLeuGluLeuIleLysTyrLeuAsnValValGluGlnLeuLys 67
360 ACTGATCTTGAGCTCATATAAATACCTAAATAATGTGGTGAACAACAGAA 409
67 sAspTrpLeuTyrLysCysSerValGlnLysLeuValValIleSerA 84
410 AGATTGGTTATACAAAGTGTTCAGTTTCAGAACTGGTTGTTAGTTATCTCAA 459
84 snlLeuSerGlyGluValLeuGluArgTrpGlnPheAspIleGluCys 100
460 ATATTGAAGTGTGTGAGTCTCTGGAAGATGGCAGTTTGTATATTGAGTGT 509
101 AspLysThrAlaLysAspSerAlaProArgGluLysSerGlnLysAl 117
510 GACAAGACTGCAAAAGATGACAGTGCACCCAGAGAAAAGTCTCAGAAGC 559
117 aileGlnAspGluIleArgSerValIleArgGlnIleThrAlaThrValT 134
560 TATCCAGATGAATCCGTTTCAGTGCATGATCAGACATCAGCTACGGTGA 609
134 hrPheLeuProLeuLeuGluValSerCysSerPheAspLeuLeuIleTyr 150
610 CATTTCTGCCACTCTTGGAGTCTTCTTTCATTTGATCTGCTGATTTAT 659
151 ThrAspLysLeuValValProGluLysTrpGluSerGlyProG1 167
660 ACAGACAAAGATTTGGTTGTACCTGAAATATGGGAAGATCGGGACCACA 709
167 nPheIleThrAsnSerGluGluValArgLeuArgSerPheThrThrI 184
710 GTTATTACCAATCTGAGGAGTCCGCCCTTCGTTCAATTACTACTACAA 759
184 leHisLysValAsnSerMetValAlaTyrLysIleProValAsnAsp 199
760 TCCACAAAGTAAATAGCATGTGGCTTACAAAATTCCTGTCAATGAC 806

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seq\_name: /cgn2\_6/ptodata/2/pna/US6021\_COMB.seq:us-60-213-359-4179

seq\_documentation\_block:

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Sequence 4179, Application US/60213359
GENERAL INFORMATION:
APPLICANT: Morris, MacDonald
APPLICANT: Lal, Preethi
APPLICANT: Diep, Dinh
TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide Polymor
TITLE OF INVENTION: Identified thereby
FILE REFERENCE: GX-0015 P
CURRENT APPLICATION NUMBER: US/60/213,359
CURRENT FILING DATE: 2000-06-21
NUMBER OF SEQ ID NOS: 7924
SOFTWARE: PERL Program
SEQ ID NO 4179
LENGTH: 1505
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: Incyte ID No: 199471.2
US-60-213-359-4179

```

alignment\_scores:

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Quality: 1010.00 Length: 199
Ratio: 5.075 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

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alignment\_block:

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US-09-352-570-2 x US-60-213-359-4179
align seg 1/1 to: US-60-213-359-4179 from: 1 to: 1505

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1 ArgGluGlnGlyIleThrIleuArgGlySerAlaGluIleValalaGluPh 17
210 CGGAGCAGGGAATACCCCTGCGGGAGCGCGAAATCGTGGCCGAGTT 259
17 ePheSerPheGlyIleAsnSerIleLeuTyrGlnArgGlyIleTyrPros 34
260 CTCTCTCATTCGGCATCAACAGCATTTATATCAGCGTGGCATATATCAT 309
34 erGluThrPheThrArgValGlnLysTyrGlyLeuThrLeuLeuValThr 50
310 CTGAACCTTTTACTCGAGTGCAGAAATACGAGCTCACCTTGTCTGTAAT 359
51 ThrAspLeuGluLeuIleLysTyrLeuAsnValValGluGlnLeuLys 67
360 ACTGATCTTGAGCTCATATAAATACCTAAATAATGTGGTGAACAACAGT 409
67 sAspTrpLeuTyrLysCysSerValGlnLysLeuValValIleSerA 84
410 AGATTGGTTATACAAAGTGTTCAGTTTCAGAACTGGTTGTTAGTTATCTCAA 459
84 snlLeuSerGlyGluValLeuGluArgTrpGlnPheAspIleGluCys 100
460 ATATTGAAGTGTGTGAGTCTCTGGAAGATGGCAGTTTGTATATTGAGTGT 509
101 AspLysThrAlaLysAspSerAlaProArgGluLysSerGlnLysAl 117
510 GACAAGACTGCAAAAGATGACAGTGCACCCAGAGAAAAGTCTCAGAAGC 559
117 aileGlnAspGluIleArgSerValIleArgGlnIleThrAlaThrValT 134
560 TATCCAGATGAATCCGTTTCAGTGCATGATCAGACATCAGCTACGGTGA 609
134 hrPheLeuProLeuLeuGluValSerCysSerPheAspLeuLeuIleTyr 150
610 CATTTCTGCCACTCTTGGAGTCTTCTTTCATTTGATCTGCTGATTTAT 659
151 ThrAspLysLeuValValProGluLysTrpGluSerGlyProG1 167
660 ACAGACAAAGATTTGGTTGTACCTGAAATATGGGAAGATCGGGACCACA 709
167 nPheIleThrAsnSerGluGluValArgLeuArgSerPheThrThrI 184
710 GTTATTACCAATCTGAGGAGTCCGCCCTTCGTTCAATTACTACTACAA 759
184 leHisLysValAsnSerMetValAlaTyrLysIleProValAsnAsp 199
760 TCCACAAAGTAAATAGCATGTGGCTTACAAAATTCCTGTCAATGAC 806

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seq\_name: /cgn2\_6/ptodata/2/pna/US6023\_COMB.seq:us-60-238-331-155

seq\_documentation\_block:

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Sequence 155, Application US/60238331
GENERAL INFORMATION:
APPLICANT: Chen, Huei-Mei
TITLE OF INVENTION: GENES EXPRESSED IN BREAST CANCER
FILE REFERENCE: PA-0037 P
CURRENT APPLICATION NUMBER: US/60/238,331
CURRENT FILING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 194
SOFTWARE: PERL Program
SEQ ID NO 155
LENGTH: 1505
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: Incyte ID No: 199471.2
US-60-238-331-155

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alignment\_scores:

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Quality: 1010.00 Length: 199
Ratio: 5.075 Gaps: 0

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Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:  
US-09-352-570-2 x US-60-238-331-155

Align seg 1/1 to: US-60-238-331-155 from: 1 to: 1505

```

1 ArgGluGlnGlyIleThrLeuArgGlySerAlaGluIleValAlaGluPh 17
210 CGGGAGCAGGGAATCACCTCGCGGGAGCGCGAAATCGTGCGCGAGTT 259
17 ePheSerPheGlyIleAsnSerIleLeuTyrGlnArgGlyIleTyrPro 34
260 CTTCTCATTCGGCATCAACAGCATTTTATATCAGCGTGCGCATATCAT 309
34 exGluThrPheThrArgValGlnLysTyrGlyLeuThrLeuValThr 50
310 CTGAAACCTTTACTCGAGTGCAGAAATACGGACTCACCTTGCTGTAACT 359
51 ThrAspLeuGluLeuIleLysTyrLeuAsnValValGluGlnLeu 67
360 ACTGATCTTGAGCTCATATAAAATACCTAAATATGTGGTGAACAAC 409
67 sAspTrpLeuTyrLysCysSerValGlnLysLeuValValIleSer 84
410 AGATTGGTTATACAGTGTTCAGTTCAGAAACTGGTTGATTTACTCAA 459
84 snIleGluSerGlyGluValLeuGluArgTrpGlnPheAspIleGlu 100
460 ATATTGAAAGTGGTGGAGTCTCGGAAAGATGCGAGTTTCATATTGAGT 509
101 AspLysThrAlaLysAspSerAlaProArgGluLysSerGlnLys 117
510 GACAGACTGCAAAAGATACAGTGCACCCAGAGAAAGTCTCAGAAAGC 559
117 alIeGlnAspGluIleArgSerValIleArgGlnIleThrAlaThr 134
560 TATCCAGGATGAATCCGTCAGTGATCAGACAGATCAGACTACGGTGA 609
134 hPheLeuProLeuLeuGluValSerCysSerPheAspLeuLeuTyr 150
610 CATTTCTGCACCTGTGGAGTTTCTTGTTCATTTGATCTGCTGATTAT 659
151 ThrAspLysAspLeuValProGluLysTrpGluLysArgGlyPro 167
660 ACAGACAAGATTGTTGTTACTGAAATGGAGAGTGGGAGTGGGACCACA 709
167 nPheIleThrAsnSerGluGluValArgLeuArgSerPheThrThr 184
710 GTTTATTACCAATTCGTAGGAAGTCCGCCCTTCGTTCAITTTACTACA 759
184 leHisLysValAsnSerMetValAlaTyrLysIleProValAsn 199
760 TCCAAAGTAATAAGCATGTGGTGGCTACAAAATTCCTGTCATGAC 806

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eq\_name: /cgn2\_5/ptodata/2/pna/US096B\_COMB.seq:US-09-693-036-3

eq\_documentation\_block:  
Sequence 3, Application us/09693036  
GENERAL INFORMATION:  
APPLICANT: Tang, Y. Tom  
APPLICANT: Liu, Chenghua  
APPLICANT: Zhou, Ping  
APPLICANT: Asundi, Vinod  
APPLICANT: Yang, Yonghong  
APPLICANT: Zhao, Qing A.  
APPLICANT: Ren, Feiyan  
APPLICANT: Xue, Aidong J.  
APPLICANT: Zhang, Jie  
APPLICANT: Drmanac, Radoje T.  
TITLE OF INVENTION: Novel Nucleic Acids and  
TITLE OF INVENTION: Polypeptides  
FILE REFERENCE: 784CIP2E

CURRENT APPLICATION NUMBER: US/09/693,036  
CURRENT FILING DATE: 2000-10-19  
PRIOR APPLICATION NUMBER: 09/552,317  
PRIOR FILING DATE: 2000-04-25  
PRIOR APPLICATION NUMBER: 09/488,725  
PRIOR FILING DATE: 2000-01-21  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: pt\_FL\_genes Version 2.0  
SEQ ID NO 3  
LENGTH: 2131  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (104)..(733)  
US-09-693-036-3

alignment\_scores:  
Quality: 1010.00 Length: 199  
Ratio: 5.075 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:  
US-09-352-570-2 x US-09-693-036-3/rev

Align seg 1/1 to reverse of: US-09-693-036-3 from: 1 to: 2131

```

1 ArgGluGlnGlyIleThrLeuArgGlySerAlaGluIleValAlaGluPh 17
2080 CGGGAGCAGGGAATCACCTCGCGGGAGCGCGAAATCGTGCGCGAGTT 2031
17 ePheSerPheGlyIleAsnSerIleLeuTyrGlnArgGlyIleTyrPro 34
2030 CTTCTCATTCGGCATCAACAGCATTTTATATCAGCGTGCGCATATCAT 1981
34 exGluThrPheThrArgValGlnLysTyrGlyLeuThrLeuValThr 50
1980 CTGAAACCTTTACTCGAGTGCAGAAATACGGACTCACCTTGCTGTAACT 1931
51 ThrAspLeuGluLeuIleLysTyrLeuAsnValValGluGlnLeu 67
1930 ACTGATCTTGAGCTCATATAAAATACCTAAATATGTGGTGAACAAC 1881
67 sAspTrpLeuTyrLysCysSerValGlnLysLeuValValIleSer 84
1880 AGATTGGTTATACAGTGTTCAGTTCAGAAACTGGTTGATTTACTCAA 1831
84 snIleGluSerGlyGluValLeuGluArgTrpGlnPheAspIleGlu 100
1830 ATATTGAAAGTGGTGGAGTCTCGGAAAGATGCGAGTTTGATATTGAGT 1781
101 AspLysThrAlaLysAspSerAlaProArgGluLysSerGlnLys 117
1780 GACAAGACTGCAAAAGATGACAGTGCACCCAGAGAAAGTCTCAGAAAGC 1731
117 alIeGlnAspGluIleArgSerValIleArgGlnIleThrAlaThr 134
1730 TATCCAGGATGAATCCGTTGAGTGCAGATCAGACATCAGACTACGGTGA 1681
134 hPheLeuProLeuLeuGluValSerCysSerPheAspLeuLeuTyr 150
1680 CATTTCTGCACCTGTGGAGTTTCTTGTTCATTTGATCTGCTGATTAT 1631
151 ThrAspLysAspLeuValProGluLysTrpGluGluSerGlyPro 167
1630 ACAGACAAGATTGTTGTTACTGAAATGGAGAGTGGGAGTGGGACCACA 1581
167 nPheIleThrAsnSerGluGluValArgLeuArgSerPheThrThr 184
1580 GTTTATTACCAATTCGTAGGAAGTGGCCTTCGTTCAITTTACTACA 1531
184 leHisLysValAsnSerMetValAlaTyrLysIleProValAsn 199

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|||||
1530 TCACAAAGTAATAGCATGGTGGCCCTACAAATTCCTGTCATGAC 1484

seq_name: /cgn2_6/ptodata/2/pna/US093_COMB.seq:US-09-352-570-3
seq_documentation_block:
; Sequence 3, Application US/09352570
; GENERAL INFORMATION:
; APPLICANT: Michael E. Mendelsohn
; TITLE OF INVENTION: METHOD FOR ASSAYING COMPOUNDS AFFECTING
; FILE OF INVENTION: CELL DIVISION
; FILE REFERENCE: 00398/506001
; CURRENT APPLICATION NUMBER: US/09/352,570
; CURRENT FILING DATE: 1999-07-13
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Ovis aries
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(600)
; 3-09-352-570-3

alignment_scores:
  Quality: 991.00      Length: 199
  Ratio: 5.005         Gaps: 0
  Percent Similarity: 99.497  Percent Identity: 97.990

alignment_block:
US-09-352-570-2 x US-09-352-570-3

Align seg 1/1 to: US-09-352-570-3 from: 1 to: 600

1  ArgGluGlnGlyIleThrLeuArgGlySerAlaGluIleValAlaGluPh 17
|||||
1  CGGGAGCAAGCATACCTTCGCGGGAGCGCGAGATCGTGGCCGAGTT 50
|||||
17  ePheSerPheGlyIleAsnSerIleLeuTyrGlnArgGlyIleTyrPro 34
|||||
51  CTCTCTATTGGTATCAACAGTATTTATATCATGCGTGGCATATATCAT 100
|||||
34  erGluThrPheThrArgValGlnLysTyrGlyLeuThrLeuValThr 50
|||||
101 CGGAAACCTTTACTCGAGTCGAGAAATATGAGTCACTACCTTGTGTA 150
|||||
51  ThrAspLeuGluLeuIleLysTyrLeuAsnValValGluGlnLeuLy 67
|||||
151 ACTGATCCTGAGTCAATAAATACCTAAATATGTGGTGGATCACTAAA 200
|||||
67  sAspTrpLeuTyrLysCysSerValGlnLysLeuValValIleSerA 84
|||||
201 AGAATGGTTATCAAGTGTTCAGTTCAGAAACTGGTGTAGTCACTCAA 250
|||||
84  snIleGluSerGlyGluValLeuGluArgTrpGlnPheAspIleGluCys 100
|||||
251 ATATTGAAAGTCGAGAGGTCCTTGAAGATGGCAGTTTGATATGAGTGT 300
|||||
101 AspLysThrAlaLysAspSerAlaProArgGluLysSerGlnLysAl 117
|||||
301 GACAAGACTCCAAAGATGACATGTCACCCAGAGAAAGTCTCAGAAGC 350
|||||
117  alleGlnAspGluIleArgSerValIleArgGlnIleThrAlaThrVal 134
|||||
351 TATCCAAGATGAATCGTTCAGTGTATCAGACAGATCAGAGTACAGTAA 400
|||||
134  hrPheLeuProLeuLeuGluValSerCysSerPheAspLeuIleTyr 150
|||||
401 CATTTCTGCCACGTGTGGAAGTTCTTGTTCATTTGATCTCTCTATTAT 450
|||||
151  ThrAspLysAspLeuValValProGluLysTrpGluGluSerGlyProG 167
```

```
|||||
451 ACAGACAAAGATCTGTTGTTACCTGAGAAATGGGAAGAGTCCGGACCACA 500
|||||
167  nPheIleThrAsnSerGluGluValArgLeuArgSerPheThrThrI 184
|||||
501 GTTCATTAGCAATTCCTGAAGAAGTTCGTTCTGTTCACTACTACTACAA 550
|||||
184  leHisLysValAsnSerMetValAlaTyrLysIleProValAsnAsp 199
|||||
551 TTCACAAAGTAATAGCATGGTGGCTACAAATTCCTGTCATGAC 597
|||||

seq_name: /cgn2_6/ptodata/2/pna/US095B_COMB.seq:US-09-540-229-121335
seq_documentation_block:
; Sequence 121335, Application US/09540229
; GENERAL INFORMATION:
; APPLICANT: Seilhamer, Jeffrey J.
; APPLICANT: Deleageane, Angelo M.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Stuve, Laura L.
; APPLICANT: Mullahy, Sara J.
; APPLICANT: Naughton, Rebecca E.
; TITLE OF INVENTION: POLYNUCLEOTIDES OF NERVOUS SYSTEM AND SENSORY ORGANS
; FILE REFERENCE: PD-1033 CIP
; CURRENT APPLICATION NUMBER: US/09/540,229
; CURRENT FILING DATE: 2000-03-31
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 193582
; SOFTWARE: PERL Program
; SEQ ID NO 121335
; LENGTH: 527
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: hu01238306
; US-09-540-229-121335
```

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alignment_scores:
  Quality: 789.00      Length: 163
  Ratio: 4.931         Gaps: 1
  Percent Similarity: 98.160  Percent Identity: 96.933

alignment_block:
US-09-352-570-2 x US-09-540-229-121335

Align seg 1/1 to: US-09-540-229-121335 from: 1 to: 527

20  PheGlyIleAsnSerIleLeuTyrGlnArgGlyIleTyrProSer Glut 36
|||||
39  TTCGGCATCAACAGCAATTTATATCAGCGTGGCATATATTCATCTTAAAA 88
|||||
36  hrPheThrArgValGlnLysTyrGlyLeuThrLeuValThrAsp 52
|||||
89  CTTTAAATTCGAGTGCAGAAATACGGACTCACCTTGCTTGAATACTGAT 138
|||||
53  LeuGluLeuIleLysTyrLeuAsnValValGluGlnLeuLysAspTr 69
|||||
139 CTTGAGCTCATAAATACCTAAATAATGTGGTGAACAACACTGAAAGATTG 188
|||||
69  pleuTyrLysCysSerValGlnLysLeuValValIleSerAsnIleG 86
|||||
189 GTTATACAAGTGTTCAGTTCAGAAACTGGTGTGATTAATCTCAATATTG 238
|||||
86  luSerGlyGluValLeuGluArgTrpGlnPheAspIleGluCysAspLys 102
|||||
239 AAAGTGGTGAAGTCTTGGAAAGATGCGAGTTTGATTTGAGTGTGACAAG 288
|||||
103 ThrAlaLysAspSerAlaProArgGluLysSerGlnLysAlaIleG 119
|||||
289 ACTGCAAAAGATGACAGTGCACCCAGAGAAAGTCTCAGAAAGCTATCCA 338
```

119 nAspGluLeuValSerGlyValLeuValGluValThrAlaThrValThrPheL 136  
 |||||  
 339 GGATGAATCCGTTCAAGTATCAGACAGATCACAGTACAGGTTGACATTTC 388  
 |||||  
 136 euProLeuLeuValSerGlyValLeuValGluValThrAlaThrValThrPheL 152  
 |||||  
 389 TGCCACTGTGTGAAGTCTTCTTCTTCAATTTGATCTGCTGATTATACAGAC 438  
 |||||  
 133 LysAspLeuValValProGluLysTrpGluGluSerGlyProGluPheL 169  
 |||||  
 439 AAAGATTTGGTTGTACCTGAAATGGAAGAGTGGGAGGAGTGGGACCACTTTAT 488  
 |||||  
 169 eThrAsnSerGluGluValArgLeuValSerPheThr 181  
 |||||  
 489 TACCATTCTGAGGAGTCCGCTTCGTTCAATTACT 525  
 |||||

seq\_name: /cgn2\_6/ptodata/2/pna/us097\_COMB.seq:US-09-726-805-585

seq\_documentation\_block:  
 ; Sequence 585, Application US/09726805  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gearing, David P.  
 ; APPLICANT: Holtzman, Douglas A.  
 ; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES  
 ; TITLE OF INVENTION: THEREFOR  
 ; FILE REFERENCE: 1600,2017-001  
 ; CURRENT APPLICATION NUMBER: US/09/726,805  
 ; CURRENT FILING DATE: 2000-11-30  
 ; PRIOR APPLICATION NUMBER: 60/168,140  
 ; PRIOR FILING DATE: 1999-11-30  
 ; NUMBER OF SEQ ID NOS: 2158  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 585  
 ; LENGTH: 607  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: (1)..(607)  
 ; OTHER INFORMATION: n = A,T,C or G  
 ; S-09-726-805-585

alignment\_scores:  
 Quality: 673.00 Length: 160  
 Ratio: 4.437 Gaps: 1  
 Percent Similarity: 94.375 Percent Identity: 92.500

alignment\_block:  
 US-09-352-570-2 x US-09-726-805-585 ..

Align seg 1/1 to: US-09-726-805-585 from: 1 to: 607

1 ArgGluGlnGlyIleThrLeuArgGlySerAlaGluIleValAlaGluPh 17  
 |||||  
 128 CGGAGCAGGGAATCACCTCGCGGGAGCGCGAAATCGTGGCGAGTT 177  
 |||||  
 17 ePheSerPheGlyIleAsnSerIleLeuTyrglnArgGlyIleTyros 34  
 |||||  
 178 CTTTCATTCGCGATCAACAGCATTTTATATCAGCGTGGCATATCATC 227  
 |||||  
 34 erGluThrPheThrArgValGlnLysTyrglyLeuThrLeuValThr 50  
 |||||  
 228 CTGAACCTTTACTCGAGTGCAGAAATACGACATCACCTTCGTTGTA 277  
 |||||  
 51 ThrAspLeuGluLeuIleTyrglyLeuAsnValValGluGlnLeuLy 67  
 |||||  
 278 ACTGATCTGAGCTCATAAATACCTAAATAATGTGGGAACTGAA 327  
 |||||  
 67 sasPTrLeuTyrglyCysSerValGlnLysLeuValValIleSera 84  
 |||||  
 328 AGATGGTTATACAAGTCTCAGTTTCAGAAATCGTTGTAGTTATCTCAA 377  
 |||||

84 snileGlu.SerGlyGluValLeuGluArgTrpGlnPheAspIleGluCy 100  
 |||||  
 378 ATATTGAAAGTGGTGAAGTCTCGAAAGATGGCAGTTTGATATGAATG 427  
 |||||  
 100 sAspLysThrAlaLysAspSerAlaProArgGluLysSerGlnLysA 117  
 |||||  
 428 TGACAAGACTGCNAAAGATGACAGTTGCACCAAGAGA.AAATCTCAGA 476  
 |||||  
 117 laileGlnAspGluIleArgSerValIleArgGlnIleThrAlaThrVal 133  
 |||||  
 477 CTANCCAGGATGAATCCGTTTCAGTGATCAGACAGATCACAGCTAC 526  
 |||||  
 134 ThrPheLeuProLeuGluValSerCysSerPheAspLeuIleTy 150  
 |||||  
 527 GACTTTCGCCACCTGTGGAATTCCTGTTCAATT.GATCTGCCAATTA 575  
 |||||  
 150 rThrAspLysAspLeuValValProGlu 159  
 |||||  
 576 TACANACAAAGATTGGGTTGTTCTCTGAA 603  
 |||||

seq\_name: /cgn2\_6/ptodata/2/pna/us092\_COMB.seq:US-09-235-076-13432

seq\_documentation\_block:  
 ; Sequence 13432, Application US/09235076  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hysq, Inc.  
 ; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
 ; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES,  
 ; FILE REFERENCE: 20411-756  
 ; CURRENT APPLICATION NUMBER: US/09/235,076  
 ; CURRENT FILING DATE: 1999-01-20  
 ; NUMBER OF SEQ ID NOS: 38054  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 13432  
 ; LENGTH: 439  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: (1)..(439)  
 ; OTHER INFORMATION: n = A,T,C or G  
 ; US-09-235-076-13432

alignment\_scores:  
 Quality: 666.00 Length: 133  
 Ratio: 5.045 Gaps: 0  
 Percent Similarity: 99.248 Percent Identity: 98.496

alignment\_block:  
 US-09-352-570-2 x US-09-235-076-13432 ..

Align seg 1/1 to: US-09-235-076-13432 from: 1 to: 439

35 GluThrPheThrArgValGlnLysTyrglyLeuThrLeuValThrTh 51  
 |||||  
 39 GAAACCTTTACTCGAGGCGAGAAATACGGACTCACCTTGCTGTGA 88  
 |||||  
 51 rAspLeuGluLeuIleLysTyrglyLeuAsnValValGluGlnLeuLysA 68  
 |||||  
 89 TGATCTTGAGCTCAATAAATACCTAAATAAGGTGGTGAACACTGAA 138  
 |||||  
 68 sPTrLeuTyrglyCysSerValGlnLysLeuValValIleSerAsn 84  
 |||||  
 139 ATTGGTTATACAGTGTTCAGTTCAGAAATCGGTTGTAGTTATCTCA 188  
 |||||  
 85 IleGluSerGlyGluValLeuGluArgTrpGlnPheAspIleGluCysA 101  
 |||||  
 189 ATTCAAAGTGGTGAAGTCTCGAAAGATGGCAGTTTGATATGAGTGA 238  
 |||||  
 101 pLysThrAlaLysAspSerAlaProArgGluLysSerGlnLysAlaI 118  
 |||||  
 239 CAAGACTGCAAAAGATGACAGTGCACCCAGAGAAAGTCTCAGAAAGCTA 288  
 |||||



```

118 leGlnaspGluileArgSerValileArgGlnileThrAlaThrValThr 134
|||||
289 TCAGGATGAATCCGTTTCAGTATCAGACAGATCACAGTACGGTGACA 338
|||||
135 PheLeuProLeuLeuGluValSerCysSerPheAspLeuLeuileYrTh 151
|||||
339 TTCTGCCACTGTGGAAGTTCTTGTTCATTGATCTGCTGATTATAC 388
|||||
151 rAspLysAspLeuValProGluLysTrpGluGluSerGlyProGln 167
|||||
389 AGACAAAGATTGGTTGTACCTGAAATGGAAGAGTCGGGACCACAG 437
|||||

```

seq\_name: /cgn2\_6/ptodata/2/pna/US092\_COMB.seq:US-09-248-797-36033

```

seq_documentation_block:
; Sequence 36033, Application US/09248797
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-764
; CURRENT APPLICATION NUMBER: US/09/248,797
; CURRENT FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 48909
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 36033
; LENGTH: 439
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; LOCATION: (1)...(439)
; OTHER INFORMATION: n = A,T,C or G
;S-09-248-797-36033

```

```

alignment_scores:
Quality: 666.00 Length: 133
Ratio: 5.045 Gaps: 0
Percent Similarity: 99.248 Percent Identity: 98.496

alignment_block:
US-09-352-570-2 x US-09-248-797-36033

```

```

Align seg 1/1 to: US-09-248-797-36033 from: 1 to: 439

35 GluThrPheThrArgValGlnLysTyrglyLeuThrLeuLeuValThrTh 51
|||||
39 GAAACCTTTACTCGAGGCGAAGATACGGACTCACCTTGTCTTAACACTAC 88
|||||
51 rAspLeuGluLeuileLysTyrglyLeuAsnValValGluGlnLeuLysA 68
|||||
89 TGATCTTGAGCTCATAAATACCTAAATAAGGTGGTGAACAACTGAAAG 138
|||||
68 sPrpLeuTyrlsCysSerValGlnLysLeuValValValIleSerAsn 84
|||||
139 ATTGGTTATACAGTGTTCAGTTTCAGAACTGGTTGTATCTCAAAAT 188
|||||
85 IleGluSerGlyGluValLeuGluArgTrpGlnPheAspIleGluCysAs 101
|||||
189 ATTGAAAGTGTGAGTCTCGGAAAGATGCGAGTTTGATATTGAGTGTA 238
|||||
101 pLysThrAlaLysAspSerAlaProArgGluLysSerGlnLysAlaI 118
|||||
239 CAAGACTGCAAAAGATGACAGTGCACCCAGAGAAAAGTCTCAGAAAAGCTA 288
|||||
118 leGlnAspGluileArgSerValileArgGlnileThrAlaThrValThr 134
|||||
289 TCAGGATGAATCCGTTTCAGTATCAGACAGATCACAGTACGGTGACA 338
|||||
135 PheLeuProLeuLeuGluValSerCysSerPheAspLeuLeuileYrTh 151
|||||

```

```

339. TTCTGCCACTGTGGAAGTTCTTGTTCATTGATCTGCTGATTATAC 388
|||||
151 rAspLysAspLeuValProGluLysTrpGluGluSerGlyProGln 167
|||||
389 AGACAAAGATTGGTTGTACCTGAAATGGAAGAGTCGGGACCACAG 437
|||||

```

seq\_name: /cgn2\_6/ptodata/2/pna/US093\_COMB.seq:US-09-332-782-13432

```

seq_documentation_block:
; Sequence 13432, Application US/09332782A
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/332,782A
; CURRENT FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13432
; LENGTH: 439
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; LOCATION: (1)...(439)
; OTHER INFORMATION: n = A,T,C or G
;US-09-332-782-13432

```

```

alignment_scores:
Quality: 666.00 Length: 133
Ratio: 5.045 Gaps: 0
Percent Similarity: 99.248 Percent Identity: 98.496

alignment_block:
US-09-352-570-2 x US-09-332-782-13432

```

```

Align seg 1/1 to: US-09-332-782-13432 from: 1 to: 439

35 GluThrPheThrArgValGlnLysTyrglyLeuThrLeuLeuValThrTh 51
|||||
39 GAAACCTTTACTCGAGGCGAAGATACGGACTCACCTTGTCTTAACACTAC 88
|||||
51 rAspLeuGluLeuileLysTyrglyLeuAsnValValGluGlnLeuLysA 68
|||||
89 TGATCTTGAGCTCATAAATACCTAAATAAGGTGGTGAACAACTGAAAG 138
|||||
68 sPrpLeuTyrlsCysSerValGlnLysLeuValValValIleSerAsn 84
|||||
139 ATTGGTTATACAGTGTTCAGTTTCAGAACTGGTTGTATCTCAAAAT 188
|||||
85 IleGluSerGlyGluValLeuGluArgTrpGlnPheAspIleGluCysAs 101
|||||
189 ATTGAAAGTGTGAGTCTCGGAAAGATGCGAGTTTGATATTGAGTGTA 238
|||||
101 pLysThrAlaLysAspSerAlaProArgGluLysSerGlnLysAlaI 118
|||||
239 CAAGACTGCAAAAGATGACAGTGCACCCAGAGAAAAGTCTCAGAAAAGCTA 288
|||||
118 leGlnAspGluileArgSerValileArgGlnileThrAlaThrValThr 134
|||||
289 TCAGGATGAATCCGTTTCAGTATCAGACAGATCACAGTACGGTGACA 338
|||||
135 PheLeuProLeuLeuGluValSerCysSerPheAspLeuLeuileYrTh 151
|||||
339. TTCTGCCACTGTGGAAGTTCTTGTTCATTGATCTGCTGATTATAC 388
|||||
151 rAspLysAspLeuValProGluLysTrpGluGluSerGlyProGln 167
|||||
389 AGACAAAGATTGGTTGTACCTGAAATGGAAGAGTCGGGACCACAG 437
|||||

```

seq\_name: /cgn2\_6/ptodata/2/pna/US093\_COMB.seq:US-09-332-782-11844

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eq_documentation_block:
Sequence 11844, Application US/09332782
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-754CON1
CURRENT APPLICATION NUMBER: US/09/332,782
CURRENT FILING DATE: 1999-06-14
EARLIER APPLICATION NUMBER: US 09/181,430
EARLIER FILING DATE: 1998-10-28
NUMBER OF SEQ ID NOS: 21027
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 11844
LENGTH: 391
TYPE: DNA
ORGANISM: Homo sapiens
S-09-332-782-11844

alignment_scores:
Quality: 574.00 Length: 116
Ratio: 5.035 Gaps: 0
Percent Similarity: 98.276 Percent Identity: 97.414

alignment_block:
US-09-352-570-2 x US-09-332-782-11844
Align seg 1/1 to: US-09-332-782-11844 from: 1 to: 391
1 ArgGluGlnGlyIleThrLeuArgGlySerAlaGluIleValAlaGluPh 17
|||||
40 CGGGAGCAGGGAATCACCTCGCGGGAGCGCGAAATCGTGCGCGAGTT 89
17 ePheSerPheGlyIleAsnSerIleLeuTyrGlnArgGlyIleTyrPro 34
|||||
90 CTTCATTCGGCATCACAGCATTTTATATACAGCGTGCATATATCAT 139
34 erGluThrPheThrArgValGlnLysTyrGlyLeuThrLeuValThr 50
|||||
140 CTGAACCTTTACTCGAGTGCAGAAATACGGACTCACCTTGCTGTA 189
140 ThrAspLeuGluLeuIleLysTyrLeuAsnValValGluGlnLeu 67
|||||
190 ACTGATCTTGAGCTCATAAAATACCTAAATATGTGGGGAACAAC 239
67 sAspTrpLeuTyrLysCysSerValGlnLysLeuValValIleSera 84
|||||
240 AGATTGGTTATACAGTGTTCAGTTCAAAACTGGTTGATGTTACTCA 289
84 snIleGluSerGlyGluValLeuGluArgTyrGlnPheAspIleGluCys 100
|||||
290 ATATTGAAAGTGGTGGAGTCTCTGGAAGATGCGACGTTTGTATAT 339
101 AspLysThrAlaLysAspSerIleProArgGluLysSerGlnLys 116
|||||
340 GACAGACTGCAGAAAGATGACAGTGCACCCAGAGAAAGCTCAGAA 387
eq_name: /cgn2_6/ptodata/2/pna/us0959A_COMB.seq:US-09-515-694-11844

eq_documentation_block:
Sequence 11844, Application US/09515694
GENERAL INFORMATION:
APPLICANT: Arterburn, Matthew
APPLICANT: Asghari, Vida
APPLICANT: Blun, Linda
APPLICANT: Cheung, Patrick
APPLICANT: Damavandi, Simin
APPLICANT: Dickson, Mark
APPLICANT: Drake, Jim
APPLICANT: Engleman, Carrie
```

67 sasptpLeuTyrlLysCysSerValGlnLysLeuValValIleSera 84  
 240 AGATTGGTTATACAGTGTTCAGTTCAAAAGCTGGTTGATGTTCTCAA 289  
 84 snIleGluSerGlyGluValLeuGluArgTrpGlnPheAspIleGluCys 100  
 290 ATATTGAAGTGGTGGAGTCCCTGGAAGATGGCAGTTTGATATTGAGTGT 339  
 101 AspLysThrAlaLysAspSerAlaProArgGluLysSerGlnLys 116  
 340 GACAAGACTGCAAAAGATGACAGTGCACCCAGAGAAAAGCTCAGAAAAG 387

seq\_name: /cgn2\_6/ptodata/2/pna/US092\_COMB.seq:US-09-235-076-28177

seq\_documentation\_block:  
 : Sequence 28177, Application US/09235076  
 : GENERAL INFORMATION:  
 : APPLICANT: HYseq, Inc.  
 : TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
 : TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES  
 : FILE REFERENCE: 20411-736  
 : CURRENT APPLICATION NUMBER: US/09/235.076  
 : CURRENT FILING DATE: 1999-01-20  
 : NUMBER OF SEQ ID NOS: 38054  
 : SOFTWARE: FastSeq for Windows Version 3.0  
 : SEQ ID NO 28177  
 : LENGTH: 472  
 : TYPE: DNA  
 : ORGANISM: Homo sapiens  
 : FEATURE:  
 : NAME/KEY: misc\_feature  
 : LOCATION: (1)...(472)  
 : OTHER INFORMATION: n = A,T,C or G  
 : US-09-235-076-28177

alignment\_scores:  
 Quality: 572.00 Length: 112  
 Ratio: 5.107 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:  
 US-09-352-570-2 x US-09-235-076-28177  
 Align seg 1/1 to: US-09-235-076-28177 from: 1 to: 472  
 1 ArgGluGlnGlyIleThrLeuArgGlySerAlaGluIleValAlaGluPh 17  
 135 CGGAGCAGGGAATCACCTGCGGGAGCGCGAAATCGTGGCCGAGTT 184  
 17 epeSerPheGlyIleAsnSerIleLeuArgGlyIleTyProS 34  
 185 CTTCATTCGGCATCACAGCATTTTATATACAGCGTGCATATATCCAT 234  
 34 erGluThrPheThrArgValGlnLysTyGlyLeuThrLeuLeuValThr 50  
 235 CTGAACCTTTACTCGAGTGCAGAAATACGACTCACCTTGTGTAACT 284  
 51 ThrAspLeuGluLeuIleLysTyLeuAsnAsnValValGluGlnLeuLy 67  
 285 ACTGATCTTCAGCTCATAAAATACCTAAATATGTGTGGTGAACAACGAA 334  
 67 sasptpLeuTyrlLysCysSerValGlnLysLeuValValIleSera 84  
 335 AGATTGGTTATACAGTGTTCAGTTCAGAACTGGTTGATGTTCTCAA 384  
 84 snIleGluSerGlyGluValLeuGluArgTrpGlnPheAspIleGluCys 100  
 385 ATATTGAAGTGGTGGAGTCCCTGGAAGATGGCAGTTTGATATTGAGTGT 434  
 101 AspLysThrAlaLysAspSerAlaProArgGlu 112

435 GACAAGACTGCAAAAGATGACAGTGCACCCAGAGAA 470

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DM of: US-09-352-570-2 to: Issued\_Patents\_NA:\* out\_format : pfs

Date: Feb 28, 2001 10:55 AM

About: Results were produced by the GenCore software, version 4.5,  
Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:

-MODEL=frame+p2n.model  
-O=/cgn2\_1/USPTO\_Spool/US09352570/runat\_26022001\_150244\_6386/app\_query.fasta\_1.258  
-DB=Issued\_Patents\_NA -QWTF=fastap -SUFFIX=rni -GAPOP=12.000  
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPEXT=0.000 -LOOPEXT=0.000  
-GAPOP=4.500 -GAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500  
-FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500  
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Search information block:

Query: US-09-352-570-2  
Query length: 199  
Database: Issued\_Patents\_NA:\*  
Database sequences: 280836  
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Search time (sec): 25.540000

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seq\_documentation\_block:

; Sequence 3, Application US/08684024  
; Patent No. 5834298  
; GENERAL INFORMATION:  
; APPLICANT: Benzeira, Robert  
; TITLE OF INVENTION: GENE ENCODING THE HUMAN HOMOLOG OF MAD2  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper & Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/684.024  
; FILING DATE: 19-JUL-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 1747/46621-A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 278-0400  
; TELEFAX: (212) 391-0526  
; INFORMATION FOR SEQ ID NO: 3:  
; LENGTH: 618 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; US-08-684-024-3

alignment\_scores:  
Quality: 1010.00 Length: 199  
Ratio: 5.075 Gaps: 0  
Percent Similarity: 100.00 Percent Identity: 100.00

alignment\_block:

US-09-352-570-2 x US-08-684-024-3

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34 ArgGluThrArgValGlyIleThrLeuThrLeuValThr 50  
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119 CTGAACCTTTACTCGAGTCGCAAAATACGATCACCCTGCTGTAACT 168  
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269 ATATTGAAAGTGGTGGAGTCCCTGGAAGATGGCAGTTGTATTTAGTGT 318
101 AspLysThrAlaLysAspSerAlaProArgGluLysSerGlnLysAl 117
319 GACAAGACTGCAAAAGATCACAGTGCACCCAGAGAAAGTCTCAGAAAGC 368
117 alleGlnAspGluIleArgSerValIleArgGlnIleThrAlaThrVal 134
369 TATCCAGGATGAAATTCCTGACGTGATCAGACAGATCAGACGTCGGTGA 418
134 hrPheLeuProLeuGluValSerCysSerPheAspLeuLeuIleTyr 150
419 CATTCTGCACCTGTGGAGTTCCTGTTTCATTGATCTGCTGATTTAT 468
151 ThrAspLysAspLeuValProGluLysTyrGlnPheAspIleGluCys 167
469 ACAGACAAAGATTTGGTTGTACCTGAAAGATGGAGAGTCGGGACCACA 518
167 nPheIleThrAsnSerGluValArgLeuArgSerPheThrThrThrI 184
519 GTTTATTACCAATTCCTGAGGAGTGGCCTTCTGTTTCTACTACTACAA 568
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Patent No. 6096522
GENERAL INFORMATION:
APPLICANT: Beneza, Robert
TITLE OF INVENTION: GENE ENCODING THE HUMAN HOMOLOG OF MAD2
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/145,868
FILING DATE: 02-SEP-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 1747/46621-B
TELEPHONE: (212) 278-0400
TELEFAX: (212) 591-0526
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 618 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
us-09-145-868-3
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Quality: 1010.00 Length: 199
Ratio: 5.075 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
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469 ACAGACAAAGATTTGGTTGTACCTGAAAGATGGAGAGTCGGGACCACA 518
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Sequence 5, Application US/08684024
Patent No. 5834298
GENERAL INFORMATION:
APPLICANT: Beneza, Robert
TITLE OF INVENTION: GENE ENCODING THE HUMAN HOMOLOG OF MAD2
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
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  Percent Similarity: 100.000  Percent Identity: 100.000

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17 ePheSerPheGlyIleAsnSerIleLeuTy rGlnArgGlyIleTy rProS 34
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84 snIleGluSerGlyGluValIleuGluArgTrpGlnPheAspIleGluCyS 100
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302 ATATTGAAAGTGGTGAGGTCCTGGAAAGATGGCGAGTTTGATATTGAGTGT 351
|||||
101 AspLysThrAlaLysAspAspSerAlaPr oArgGluLysSerGlnLysAl 117
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352 GACAAGACTGCAAAAGATGACATGCGACCCACAGAGAAAGTCTCAGAAAGC 401
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Patent No. 5834298  
GENERAL INFORMATION:  
APPLICANT: Benzeira, Robert  
TITLE OF INVENTION: GENE ENCODING THE HUMAN HOMOLOG OF MAD2  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham LLP  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/684,024  
FILING DATE: 19-JUL-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:

NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 1747/46621-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 278-0400  
TELEFAX: (212) 391-0526  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 591 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-684-024-4  
alignment\_scores:  
Quality: 395.50 Length: 197  
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Percent Similarity: 76.142 Percent Identity: 43.147  
alignment\_block:  
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57 GTACAGCATTAATCCATTTTGTACCAAGAGGGGTATACCCACAGAGA 106  
36 hrPheThrArgValGlnLysTyrGlyLeuThrLeuValThrThrAsp 52  
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53 LeuGluLeuIleLysTyrLeuAsnValValGluGlnLysAspTrp 69  
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157 GATGAACGTGAAGATTAATTCGGAAAGATCTTCTCAAGATTACAGGTG 206  
69 lLeuTyrLysCysSerValGlnLysLeuValValIleSerAsnIleG 86  
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207 GCTTCTTCGCGAAATGCAATCAATAGTATTATGTTAGTACACAGG 256  
86 luSerGlyGluValLeuGluArgTrpGlnPheAspIleGlu..... 99  
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116 sAlaIleGlnAspGluIleArgSerValIleArgGlnIleThrAlaThr 133  
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133 alThrPheLeuProLeuLeu.....GluValSerCysSerPheAspLeu 147  
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148 LeuIleTyrThrAspLysAspLeuValValProGluLysTrpGluGlu 164  
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164 rGlyProGlnPheIleThrAsnSerGluValValArgLeuArgSerPhe 181  
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seq_documentation_block:
: Sequence 4, Application US/09145868
: Patent No. 6096522
: GENERAL INFORMATION:
: APPLICANT: Benezia, Robert
: TITLE OF INVENTION: GENE ENCODING THE HUMAN HOMOLOG OF MAD2
: NUMBER OF SEQUENCES: 9
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Cooper & Dunham LLP
: STREET: 1185 Avenue of the Americas
: CITY: New York
: STATE: New York
: COUNTRY: U.S.A.
: ZIP: 10036
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/145,868
: FILING DATE: 02-SEP-1998
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: White, John P.
: REGISTRATION NUMBER: 28,678
: REFERENCE/DOCKET NUMBER: 1747/46621-B
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 278-0400
: TELEFAX: (212) 391-0526
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 591 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: PS-09-145-868-4

```

```

alignment_scores:
    Quality: 395.50      Length: 197
    Ratio: 2.637         Gaps: 3
    Percent Similarity: 76.142    Percent Identity: 43.147

alignment_block:
    US-09-352-570-2 x US-09-145-868-4 ..

    Align seg 1/1 to: US-09-145-868-4 from: 1 to: 591

3  GlnGlyIleThrLeuArgGlySerAlaGluIleValAlaGluPhePhe 19
7  CAATCAATATCACTAAGGGTTCAACAAGCACAGTTACAGAATTTTCGA 46
19  rPheGlyIleAsnSerIleLeuTyrGlnArgGlyIleTyrProSerGlu 36
57  GTACAGCATTAATTCATTTTGTACCAAAAGAGCGGTATACCCAGCAGAAG 106
36  hrPheThrArgValGlnLysTyrGlyLeuThrLeuLeuValThrThrAsp 52
107  ATTTTCGTAACGGTGAAGAAAGTACGATCTTACGTTACTAAAGACACATGAT 156
53  LeuGlnLeuIleLysTyrLeuAsnAsnValValGluGlnLeuLysAspTr 69
157  GATGAAGCTGAAGATTACATTCCGGAATAATCTTCTACAAGTTCCAGG 206
69  pLeuTyrLysCysSerValGlnLysIleuValValIleSerAsnIleG 86
207  GCTTCTTTGGTGAAGATGCAATCAATAGTATTATGTTATGATGACAGG 256

```

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86 luSerGlyGluValLeuGluArgTrpGlnPheAspLeu..... 99
257 ATGAGGAGAGGTGGTGAAGATGCTCCTCAATGTGCAACACATTCT 306
100 CysAspLysThrAlaLysAspSerAlaProArgGluLysSerGlnLy 116
307 GCGAATAGCAACGGCAGGATGATGTGA.....GATTTAAA 344
116 salAleGlnAspLulLeArgSerValIleArgGlnIleThrAlaThrV 133
345 TACAACACATCACAATCAGAGCTTTAATCAGGCAATCACCCTCAAGG 394
133 alThrPheLeuProLeuLeu.....GluValIserCysSerPheAspLeu 147
395 TTACCTTTCTGCCCGCAACTAACAAAAAGAGTGGGTACACATTCACAGTA 444
148 LeuIleYrThrAspLysAspLeuValValProGluLysTrpGluGluSe 164
445 CTTCATATACAGACGGGATGCTAAAGTTCCGTTAGAAATGGCCGCGATC 494
164 rGlyProGlnPheIleThrAsnSerGluValArgLeuArgSerPheT 181
495 CAATAGTAAGACATACCTGATGCTGAAGTCTCAATTCAAAACATTCT 544
181 hrThrIleHisLysValAsnSerMetValAlaTyrLys 194
545 CTACCAACGATCATAAAGTTGGTGGCAGGTCAGGTATAAAA 585
seq_name: /cqn2_6/ptodata/2/ina/6_COMB.seq; US-08-961-083-217

seq_documentation_block:
; Sequence 217, Application US/08961083
; Patent No. 6159469
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
; NUMBER OF SEQUENCES: 452
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961.083
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 217:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1696 base*pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-961-083-217

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Quality: 72.50 Length: 171  
Ratio: 0.797 Gaps: 8  
Percent Similarity: 53.216 Percent Identity: 19.883

## - alignment\_block:

US-09-352-570-2 x US-08-961-083-217 ..

Align seg 1/1 to: US-08-961-083-217 from: 1 to: 1696

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29 ArgGlyIleTyrProSerGluThrPheThrArgValGlnLysTyrGlyLe 45
   :::::||||| ::::: :::::
833 AAGGTCGTCTATGCTTCAGAGCGTGTAAACAGCGCTCAGGTAATACGGA 882
   ||| ::::: ||| :::::
45 uThrLeuValThrThrAspLeuGluLeuLysTyr..... 58
   ||| ::::: ||| :::::
883 GACAAATAACCTTAAACCGCTATTGACGCTTAAACGTTGATAAAACG 932
   ||| ::::: ||| :::::
59 ..LeuAsnAsnValValGluGlnLeuLysAspTrpLeuTyrLysCysSer 74
   ||| ::::: ||| :::::
933 AATTAAACAATACGATTGACAGTGCAGAA..... 961
   ||| ::::: ||| :::::
75 ValGlnLysLeuValValValIleSerAsnIleGluSerGlyGluValle 91
   ::::: ||| :::::
962 .....ACAAAGGTAAAGAACATTACAGTGA 987
   ||| ::::: ||| :::::
91 uGluArgTyrGlnPheAspIleGluCysAspLysThrAlaLysAspAsps 108
   ::::: ||| ::::: |||
988 TAGAAGTTGGCAA....AACTCCAACTGAAGTTACAAAGGCGTGAAGAG 1034
   ||| ::::: ||| :::::
108 exAlaProArgGluLysSerGlnLysAlaIleGlnAspGluLeuArgSer 124
   ||| ::::: ||| :::::
1035 TTGCA.....GCTAATACAGATGCTAAACAAAGTGAAGTAAACGAA 1075
   ||| ::::: ||| :::::
125 ValIleArgGlnIleThrAlaThrValThrPheLeuProLeuLeuGluVa 141
   ::::: ||| ::::: |||
1076 GCTGTTGAAATAATTAACCTCAACTATTGAA.....AAATTGTTGAAT 1119
   ||| ::::: ||| :::::
141 lSerCysSerPheAspLeuIleTyrThrAspLysAspLeuValValp 158
   ||| ::::: ||| ::::: |||
1120 ATCT....GAAAGCCCAATATTACATGTACTAGTACCGATAGCAAAATAT 1166
   ||| ::::: ||| ::::: |||
158 roGluLysTrpGluGluSerGlyProGlnPheIleThrAsnSerGluGlu 174
   ||| ::::: ||| ::::: |||
1167 TGAACGT...GAAGCTGTTGCTAAGTATATCTAGAAATCAAAACAAA 1213
   ||| ::::: ||| ::::: |||
175 ValArgLeuArgSerPheThrThrThrIleHisLys.....Va 187
   ::::: ||| ::::: |||
1214 ACAAATAATCAATCAATCACAGTGAATTGAAAGAGGAGAGAGAGTTAT 1263
   ||| ::::: ||| ::::: |||
187 lAsnSerMetVal 191
   ||| ::::: ||| ::::: |||
1264 TAATACTGTAGTC 1276
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eq\_name: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq:US-08-261-206A-71

## -eq\_documentation\_block:

Sequence 71. Application US/08261206A

Patent No. 5574007

## GENERAL INFORMATION:

APPLICANT: Zushi, Mitichitaka

APPLICANT: Gomi, Komakazu

APPLICANT: Yamamoto, Shuji

APPLICANT: Suzuki, Koji

APPLICANT: Matsuda, Akio

TITLE OF INVENTION: A Polypeptide Capable of Interacting

with Thrombin

NUMBER OF SEQUENCES: 80

CORRESPONDENCE ADDRESS:

ADDRESSEE: Birch, Stewart, Kolasch & Birch

STREET: 301 N. Washington St.

CITY: Falls Church

STATE: Virginia

COUNTRY: USA

ZIP: 22046-0747.  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/261.206A  
FILING DATE:  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/740,492  
FILING DATE: 03-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Svensson, Leonard R.  
REGISTRATION NUMBER: 30330  
REFERENCE/DOCKET NUMBER: 216-275P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-241-1300  
TELEFAX: 703-241-2848  
TELEX: 248345

INFORMATION FOR SEQ ID NO: 71:

SEQUENCE CHARACTERISTICS:

LENGTH: 3306 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

ORIGINAL SOURCE:

ORGANISM: Acremonium chrysogenum

FEATURE:

NAME/KEY: -

LOCATION: 1..3306

OTHER INFORMATION: /label= PKG\_gene

OTHER INFORMATION: /note= "Nucleotide sequence of region A in Figure 59. The sequence is presented as Figure 61."

FEATURE:

NAME/KEY: exon

LOCATION: 1252..1317

FEATURE:

NAME/KEY: exon

LOCATION: 1463..1883

FEATURE:

NAME/KEY: exon

LOCATION: 1948..2715

FEATURE:

NAME/KEY: CDS

LOCATION: join(1252..1317, 1463..1883, 1948..2714)

US-08-261-206A-71

## alignment\_scores:

Quality: 72.50 Length: 84

Ratio: 1.480 Gaps: 3

Percent Similarity: 58.333 Percent Identity: 32.143

## alignment\_block:

US-09-352-570-2 x US-08-261-206A-71 ..

Align seg 1/1 to: US-08-261-206A-71 from: 1 to: 3306

42 LysTyrGlyLeuThrLeuValThrThrAspLeuGluLeuLysTyr 58

||||| ::::: ||| ::::: |||

1619 AAGTACTCGCTGCAGCCCGTGTCCCG.....GAGCTCGAGAGCT 1659

||||| ::::: ||| ::::: |||

58 rLeuAsnAsnValValGluGlnLeuLysAspTrpLeuTyrLysCysSerV 75

||||| ::::: ||| ::::: |||

1660 GCTCGGCAAGAGCGTCACTTTCCGCCCGCAC.....TCGCTCG 1697

||||| ::::: ||| ::::: |||

75 aGlnLysLeuValValValIleSerAsnIleGluSerGlyGluVal... 90

||||| ::::: ||| ::::: |||

1698 GCGCGAGTGTGAGGCGTTCGTGCGCAAGCGGAGCGGCGCGTGTTC 1747



```

FEATURE:
NAME/KEY: CDS
LOCATION: 183..1484
S-08-706-216-3

alignment_scores:
Quality: 72.00 Length: 135
Ratio: 0.986 Gaps: 8
Percent Similarity: 58.400 Percent Identity: 29.600

alignment_block:
US-09-352-570-2 x US-08-706-216-3 ..
Align seg 1/1 to: US-08-706-216-3 from: 1 to: 2030

7 LeuArgGlySerAlaGluLeuValAlaGluPheSerPheGlyLeuAs 23
|||||
531 TTGAGAGCGGATGCGAGAGCAGTGAAG.....GGCATAGGATCCGG 571
|||||
23 nSerIleLeuTyrGlnArgGly.....IleTyrProS 34
|||||
572 CAAAGTCCTG...AAGAGTGGCCCCCAGGATCACGTGTTTCATTAC.... 614
|||||
34 exGluThrPheThrArgValGlnLeuTyrGlyLeuThrLeuValThr 50
|||||
615 .....TTCACTGACCATGATCTACTGGAATACGTGTTTTCCTCAAT 656
|||||
51 ThrAspLeuGluLeuIleTyrLeuAsnValValGluGlnLeu 67
|||||
657 GAAGATCTTCAT...GTAAGACCTGATGAGACCATCCAT..... 695
|||||
67 sasTrpLeuTyrLysCysSerVal...GlnLysLeuValValIleS 83
|||||
696 ....TACATGTACAAACAAATGATCCGAAAGATGGTGTCTCATATTG 741
|||||
83 eAsnIleGluSerGlyGluValLeuGluArgTrpGlnPheAspLeu 99
|||||
742 AAGCCTGTGAGTCTGGTCCATGATGACACCATCCGCGATCAATCAAT 791
|||||
100 CysAspLysThrAlaLysAspSerAlaProArgGluLysSerGln 116
|||||
792 GTTATGCACTACTGCT.....GCCAACCCAGAGAGTCTCTACGC 835
|||||
116 salAlleGlnAspGluIleArgSer 124
|||||
836 CTGTTACTATGATGAGAAGAGTCC 860
|||||

eq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-206-176-5

eq_documentation_block:
Sequence 5, Application US/08206176
Patent No. 5639940
GENERAL INFORMATION:
APPLICANT: Garner, Ian
APPLICANT: Dairymple, Michael A
APPLICANT: Prunkard, Donna E
APPLICANT: Foster, Donald C
TITLE OF INVENTION: Production of Fibrinogen in Transgenic
TITLE OF INVENTION: Animals
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Zymogenetics, Inc.
STREET: 4225 Roosevelt Way, N.E.
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98105
COMPUTER READABLE FORM: disk
MEDIUM TYPE: Floppy
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/206,176
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Parker, Gary E
REGISTRATION NUMBER: 31-648
REFERENCE/DOCKET NUMBER: 93-15
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-547-8080 ext 322
TELEFAX: 206-548-2329
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 10584 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
CLONE: human fibrinogen gamma chain
FEATURE:
NAME/KEY: CDS
LOCATION: Join(1799..1876, 1973..2017, 2207..2390, 2510
LOCATION: ..2603, 4211..4341, 4645..4778, 5758..5942, 7426
LOCATION: ..7703, 9342..9571)
US-08-206-176-5

alignment_scores:
Quality: 72.00 Length: 98
Ratio: 1.220 Gaps: 4
Percent Similarity: 60.204 Percent Identity: 25.510

alignment_block:
US-09-352-570-2 x US-08-206-176-5 ..
Align seg 1/1 to: US-08-206-176-5 from: 1 to: 10564

13 IleValAlaGluPheSerPheGlyLeuAsnSerIleLeuTyrGlnAr 29
|||||
4047 TTGTAATATATATTTTACATTTTCTCAAGAAATGGAATAATTTATCAGAA 4096
|||||
29 gGlyIleTyrProSerGluThrPheThrArgValGlnLysTyrGlyLeu 46
|||||
4097 AGCACTTCTTGAAGAAATATCTTACAGTTTCCCAAGAAATATATAATTA 4146
|||||
46 hrLeu.....LeuValThrThrAspLeuGluLeuIleLysTyr 58
|||||
4147 CTCCTCTGAAAGGAATATCTTATTTTCTCTTCTTATTTTGTATCTAT 4196
|||||
59 LeuAsnAsnValValGluGlnLeuLysAspTrpLeuTyrLysCysSerVa 75
|||||
4197 GTT...TCTGTTTGTAGATATTTCCAGAA...ATATATATATCAATAAA 4240
|||||
75 gLysLeuValValValIleSerAsnIleGluSerGlyGluValLeuG 92
|||||
4241 TCAAAAGATTTGTTAACTGAAAGAGAGAGGTAGCC..... 4274
|||||
92 luArgTrpGlnPheAspIleGluCysAspTyrThrAlaLysAsp 106
|||||
4275 .....CAGCTTGAAGCACAGTGCAGGAGACCTTGCAAGAC 4310
|||||

seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-568-147B-1

seq_documentation_block:
Sequence 1, Application US/08568147B
Patent No. 5783422
GENERAL INFORMATION:
APPLICANT: Suminami, Yoshinori
APPLICANT: Kato, Hiroshi
APPLICANT: Sekiguchi, Kiyoshi
APPLICANT: Takeda, Katsumichi
TITLE OF INVENTION: DNA FRAGMENT CODING FOR SQUAMOUS CELL

```



```
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-094-889-2

alignment_scores:
  Quality: 71.50      Length: 153
  Ratio: 0.872       Gaps: 8
  Percent Similarity: 50.307   Percent Identity: 23.313

alignment_block:
US-09-352-570-2 x US-08-094-889-2 ..
Align seg 1/1 to: US-08-094-889-2 from: 1 to: 3123
57 LysTyrLeuAsnValValGluGlnLeuLysAspTrpLeuTyrLysCy 73
1394 GAGCATGCCACACAGCTGTTGAG..... 1417
73 sSerValGlnLysLeuValValIleSerAsnIleGluSerGlyGluV 90
1418 ...GTTGCAAACTGGCTGTTCCATCTCAAAATATGAAGAAGGTGTA 1463
90 alLeuGluArgTrp.....GlnPheAspIleGluCysAspLys... 102
1464 AGCTAGTCGCTGACGACACACAGATGATGATGCTGTCGCCACAGTA 1513
103 .....ThrAlaLysAspSerAlaProArgG1 112
1514 ATAAATGCTGCGTCAACCTGGCTGCCAGCTCAGACCAAGTAGCACA 1563
112 uLySerGlnLysAlaIleGlnAspGluIleArgSerValIleArgGlnI 129
1564 GGACAACATGATGCTTTAAAGGATCAGTGGGAGAAACAAGTGGCAGTTC 1613
129 leThrAlaThrValThrPheLeuProLeuLeuGlu.ValSerCysSerPh 145
1614 TCACGTGAAGCAGTGTATGACATCACTTCAGTGGGATGATTCCTCTCTGT 1663
145 eAspLeuLeuIleTyr..... 152
1454 eAspLeuLeuIleTyr..... 152
```

```
1664 TCAGAAATCATATTCGAGATGTGACAAATGTGTGATTGCTCTCCA 1713
152 spLysAspLeuValProGluLysTrp...GluGluSerGlyProGln 167
1714 AGAGGAGATGCTGATACCC.....TGGATAGAACTGCTGGGCCA... 1754
168 PheIleThrAsnSerGluGluValArgLeuArgSerPheThrThrI1 184
1755 .....TCCGAGCGCTGCAGCAGCAGATCATTCATCATTAAT 1792
184 eHisLysValAsnSerMetValAlaTyrLysIlePro 196
1793 GCAGAGATGGAAACTATGAAACTGGAGTTTATACCG 1829
seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-105-483-222
seq_documentation_block:
; Sequence 222, Application US/08105483
; Patent No. 5494807
; GENERAL INFORMATION:
; APPLICANT: Paolletti, Enzo
; TITLE OF INVENTION: GENETICALLY ENGINEERED VACCINE
; TITLE OF INVENTION: STRAIN
; NUMBER OF SEQUENCES: 462
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford
; ADDRESSEE: c/o William S. Frommer
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/105,483
; FILING DATE: 12-AUG-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/847,951
; FILING DATE: 06-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454310-2400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 222:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2356 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-105-483-222

alignment_scores:
  Quality: 71.00      Length: 138
  Ratio: 0.887       Gaps: 7
  Percent Similarity: 57.971   Percent Identity: 22.464

alignment_block:
US-09-352-570-2 x US-08-105-483-222/rev ..
Align seg 1/1 to reverse of: US-08-105-483-222 from: 1 to: 2356
52 AspLeuGluLeuIleLysTyrLeuAsnValValGluGlnLeuLysAs 68
1964 GATATTAGATCGACCAATGGTTACTAGATCTTGAGAA..... 1936
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